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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:16:16 ; Search time 22 Seconds  
(without alignments)  
492.793 Million cell updates/sec

Title: US-10-029-079-3  
Perfect score: 1166  
Sequence: 1 MKENVASATVFTLLFLNTCLNGOLPGCKPIFKCRSPNKETFCWRRPGTDGGLPTNY 210

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/2/iaa/PCTRUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1155.5	99.1	349	3	US-08-806-597A-14
2	1155.5	99.1	349	3	US-08-970-428A-14
3	1042.5	89.4	599	3	US-09-000-145-2
4	863.5	74.1	593	3	US-09-000-145-4
5	809.5	69.4	592	3	US-09-000-145-6
6	679	58.2	134	3	US-08-806-597A-8
7	679	58.2	134	3	US-08-970-428A-8
8	387	33.2	118	3	US-08-806-597A-4
9	387	33.2	118	3	US-08-970-428A-4
10	297	25.5	389	3	US-09-071-224-25
11	297	25.5	389	3	US-09-071-224-26
12	296	25.4	303	3	US-09-071-224-21
13	296	25.4	385	3	US-09-071-224-20
14	296	25.4	388	3	US-09-071-224-17
15	296	25.4	389	3	US-09-071-224-27
16	296	25.4	389	3	US-09-071-224-31
17	296	25.4	422	3	US-09-071-224-2
18	295	25.3	389	3	US-09-071-224-30
19	294	25.2	389	3	US-09-071-224-24
20	294	25.2	389	3	US-09-071-224-28
21	294	25.2	389	3	US-09-071-224-29
22	293	25.1	303	3	US-09-071-224-23
23	293	25.1	389	3	US-09-071-224-22
24	293	25.1	392	3	US-09-071-224-18
25	293	25.1	422	4	US-08-866-028-32
26	293	25.1	425	3	US-09-071-224-4
27	292	25.0	385	3	US-09-071-224-19

SEQ  
A.A. 25-349 - 14

28	292	25.0	405	3	US-09-012-072-2	Sequence 2, Appli
29	292	25.0	405	3	US-09-120-601-2	Sequence 2, Appli
30	292	25.0	425	3	US-09-071-224-6	Sequence 6, Appli
31	291.5	25.0	620	3	US-09-000-145-5	Sequence 5, Appli
32	289.5	24.8	620	3	US-09-000-145-3	Sequence 3, Appli
33	273	23.4	434	3	US-09-012-072-4	Sequence 4, Appli
34	273	23.4	434	3	US-09-120-601-4	Sequence 4, Appli
35	273	23.4	448	3	US-09-120-601-6	Sequence 6, Appli
36	262.5	22.1	620	3	US-09-000-145-1	Sequence 1, Appli
37	246	21.1	204	3	US-09-043-785-2	Sequence 2, Appli
38	237	20.3	48	3	US-08-806-597A-6	Sequence 6, Appli
39	237	20.3	48	3	US-08-970-428A-6	Sequence 6, Appli
40	227.5	19.5	148	1	US-08-224-982-3	Sequence 3, Appli
41	227.5	19.5	148	2	US-08-468-580-3	Sequence 3, Appli
42	227.5	19.5	148	3	US-08-643-212-2	Sequence 2, Appli
43	227.5	19.5	148	5	PCT-US95-03731-3	Sequence 3, Appli
44	223.5	19.2	148	1	US-08-224-982-4	Sequence 4, Appli
45	223.5	19.2	148	2	US-08-468-580-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-08-806-597A-14  
; Sequence 14, Application US/08806597A  
; Patent No. 6083714  
; GENERAL INFORMATION:  
; APPLICANT: KELLY, Paul A. and NAGANO, Makoto  
; TITLE OF INVENTION: SOLUBLE HUMAN PROLACTIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/806,597A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/012,503  
; FILING DATE: 29 February 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: KELLY=1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 349 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-806-597A-14

Query Match 99.1%; Score 1155.5; DB 3; Length 349;  
Best Local Similarity 99.5%; Pred. No. 1.8e-116;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLNGOLPGCKPIFKCRSPNKETFCWRRPGTDGGLPTNY 60  
DB 1 MKENVASATVFTLLFLNTCLNGOLPGCKPIFKCRSPNKETFCWRRPGTDGGLPTNY 60

QY 61 SLTYHREGTLMHRCPDYITGGPNCHFGKQYTSMMRTYIMVNAT-QMGSSFSDELVD 119  
 Db 61 SLTYHREGTLMHRCPDYITGGPNCHFGKQYTSMMRTYIMVNAT-QMGSSFSDELVD 120  
 QY 120 VTYIVQDPPLELAVEVKQPEDRKPYLWKSPPTLLDLKTGWFTLLYEIRLKPKEAAEW 179  
 Db 121 VTYIVQDPPLELAVEVKQPEDRKPYLWKSPPTLLDLKTGWFTLLYEIRLKPKEAAEW 180  
 QY 180 EHFAGQOTEFKILSLHFGQKYLQVRCCKPD 210  
 Db 181 EHFAGQOTEFKILSLHFGQKYLQVRCCKPD 211

## RESULT 2

US-08-970-428A-14  
 ; Sequence 14, Application US/08970428A  
 ; Patent No. 6083753  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KELLY, Paul A. and NAGANO, Makoto  
 ; TITLE OF INVENTION: SOLUBLE HUMAN PROLACTIN RECEPTORS  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/970,428A  
 ; FILING DATE: 14-NOV-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/012,503  
 ; FILING DATE: 29-FEB-1996  
 ; PRIOR APPLICATION DATA: US 08/806,597  
 ; FILING DATE: 26-FEB-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: YUN, Allen C.  
 ; REGISTRATION NUMBER: 37,971  
 ; REFERENCE/DOCKET NUMBER: KELLY=1B  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 349 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Protein

US-08-970-428A-14

A.A. 25-349 - SEQ # 14

Query Match 99.1%; Score 1155.5; DB 3; Length 349;  
 Best Local Similarity 99.5%; Pred. No. 1.8e-116;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKNVASATVFLLFLNCLLNGQLPPGKPIFKRSPNKETFTCWRRPGTGGGLPTNY 60  
 Db 1 MKNVASATVFLLFLNCLLNGQLPPGKPIFKRSPNKETFTCWRRPGTGGGLPTNY 60  
 QY 61 SLTYHREGTLMHRCPDYITGGPNCHFGKQYTSMMRTYIMVNAT-QMGSSFSDELVD 119  
 Db 61 SLTYHREGTLMHRCPDYITGGPNCHFGKQYTSMMRTYIMVNAT-QMGSSFSDELVD 120  
 QY 120 VTYIVQDPPLELAVEVKQPEDRKPYLWKSPPTLLDLKTGWFTLLYEIRLKPKEAAEW 179  
 Db 121 VTYIVQDPPLELAVEVKQPEDRKPYLWKSPPTLLDLKTGWFTLLYEIRLKPKEAAEW 180

QY 180 EHFAGQOTEFKILSLHFGQKYLQVRCCKPD 210  
 Db 181 EHFAGQOTEFKILSLHFGQKYLQVRCCKPD 211

## RESULT 3

US-09-000-145-2  
 ; Sequence 2, Application US/09000145  
 ; Patent No. 6169172  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DEVAUCHELLE, Gerrard  
 ; APPLICANT: GARNIER, Laurence  
 ; APPLICANT: CAHOREAU, Claire  
 ; APPLICANT: CERUTTI, Martine  
 ; TITLE OF INVENTION: USE OF A PROLACTIN RECEPTOR OR GROWTH HORMONE RECEPTOR  
 ; FILE REFERENCE: 0384-0047-OXPECT  
 ; CURRENT APPLICATION NUMBER: US/09/000,145  
 ; CURRENT FILING DATE: 1998-03-16  
 ; EARLIER APPLICATION NUMBER: PCT/FR96/01237  
 ; EARLIER FILING DATE: 1996-08-02  
 ; EARLIER APPLICATION NUMBER: FR 95/09420  
 ; EARLIER FILING DATE: 1995-08-02  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 599  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-000-145-2

Query Match 89.4%; Score 1042.5; DB 3; Length 599;  
 Best Local Similarity 99.5%; Pred. No. 6.1e-104;  
 Matches 187; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 24 GOLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNYSLTYHREGTLMHRCPDYITGGP 83  
 Db 1 GOLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNYSLTYHREGTLMHRCPDYITGGP 60  
 QY 84 NSCHFGKQYTSMMRTYIMVNAT-QMGSSPSDELVDVTYIVQDPPLELAVEVKQPEDR 142  
 Db 61 NSCHFGKQYTSMMRTYIMVNAT-QMGSSPSDELVDVTYIVQDPPLELAVEVKQPEDR 120  
 QY 143 KPYLWKSPPTLLDLKTGWFTLLYEIRLKPKEAAEWIHFAGQOTEFKILSLHFGQKYL 202  
 Db 121 KPYLWKSPPTLLDLKTGWFTLLYEIRLKPKEAAEWIHFAGQOTEFKILSLHFGQKYL 180  
 QY 203 VQVRCKPD 210  
 Db 181 VQVRCKPD 188

## RESULT 4

US-09-000-145-4  
 ; Sequence 4, Application US/09000145  
 ; Patent No. 6169172  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DEVAUCHELLE, Gerrard  
 ; APPLICANT: GARNIER, Laurence  
 ; APPLICANT: CAHOREAU, Claire  
 ; APPLICANT: CERUTTI, Martine  
 ; TITLE OF INVENTION: USE OF A PROLACTIN RECEPTOR OR GROWTH HORMONE RECEPTOR  
 ; FILE REFERENCE: 0384-0047-OXPECT  
 ; CURRENT APPLICATION NUMBER: US/09/000,145  
 ; CURRENT FILING DATE: 1998-03-16  
 ; EARLIER APPLICATION NUMBER: PCT/FR96/01237  
 ; EARLIER FILING DATE: 1996-08-02  
 ; EARLIER APPLICATION NUMBER: FR 95/09420  
 ; EARLIER FILING DATE: 1995-08-02  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4

; LENGTH: 593  
; TYPE: PRT  
; ORGANISM: Oryctolagus cuniculus  
US-09-000-145-4  
  
Query Match 74.1%; Score 863.5; DB 3; Length 593;  
Best Local Similarity 79.3%; Pred. No. 1.3e-84;  
Matches 149; Conservative 18; Mismatches 20; Indels 1; Gaps 1;  
  
QY 24 GQLPPGKPIFKCRSPNKTFTCWRRPGTDGGLPTNYSLYTHREGETLMHECPDYITGGP 83  
Db 1 GQSPPGKPIFKCRSPNKTFTCWRRPGTDGGLPTNYSLYTHREGETLMHECPDYITGGP 60  
  
QY 84 NSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELVDVTVIVQPPPLELAVEVKQPEDR 142  
Db 61 NSCYFSEKTSITWIIITVNATNQMGSSVSDPRYVDVTVIVQPPPLELAVEVKQPEDR 120  
  
QY 143 KPYLWIKWSPPTLIDLTGWTLLYIRLKPKEAAEWEIHFAGQQTFFKILSLHPGQKYL 202  
Db 121 KPYLWIKWSPPTLIDLTGWTLLYIRLKPKEAAEWEIHFAGQQTFFKILSLHPGQKYL 180  
  
QY 203 VQVRCKPD 210  
Db 181 VQVRCKPD 188

RESULT 5  
US-09-000-145-6  
; Sequence 6, Application US/09000145  
; Patent No. 6169172  
; GENERAL INFORMATION:  
; APPLICANT: DEVAUCHELLE, Gerard  
; APPLICANT: GARNIER, Laurence  
; APPLICANT: CAHOREAU, Claire  
; APPLICANT: CERUTTI, Martine  
; TITLE OF INVENTION: USE OF A PROLACTIN RECEPTOR OR GROWTH HORMONE RECEPTOR  
; TITLE OF INVENTION: INTRACYTOSOLIC DOMAIN FOR ACHIEVING PROTEIN SECRETION  
; FILE REFERENCE: 0384-0047-0XPCT  
; CURRENT APPLICATION NUMBER: US/09/000,145  
; CURRENT FILING DATE: 1998-03-16  
; EARLIER APPLICATION NUMBER: PCT/FR96/01237  
; EARLIER FILING DATE: 1996-08-02  
; EARLIER APPLICATION NUMBER: FR 95/09420  
; EARLIER FILING DATE: 1995-08-02  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
US-09-000-145-6

Query Match 69.4%; Score 809.5; DB 3; Length 592;  
Best Local Similarity 74.5%; Pred. No. 8.7e-79;  
Matches 140; Conservative 19; Mismatches 28; Indels 1; Gaps 1;  
  
QY 24 GQLPPGKPIFKCRSPNKTFTCWRRPGTDGGLPTNYSLYTHREGETLMHECPDYITGGP 83  
Db 1 GQSPPGKPIFKCRSPNKTFTCWRRPGTDGGLPTNYSLYTHREGETLMHECPDYITGGP 60  
  
QY 84 NSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELVDVTVIVQPPPLELAVEVKQPEDR 142  
Db 61 NSCYFSEKTSITWIIITVNATNQMGSSVSDPRYVDVTVIVQPPPLELAVEVKQPEDR 120  
  
QY 143 KPYLWIKWSPPTLIDLTGWTLLYIRLKPKEAAEWEIHFAGQQTFFKILSLHPGQKYL 202  
Db 121 KPYLWIKWSPPTLIDLTGWTLLYIRLKPKEAAEWEIHFAGQQTFFKILSLHPGQKYL 180  
  
QY 203 VQVRCKPD 210  
Db 181 VQVRCKPD 188

RESULT 6  
US-08-806-597A-8  
; Sequence 8, Application US/08806597A  
; Patent No. 6083714  
; GENERAL INFORMATION:  
; APPLICANT: KELLY, Paul A. and NAGANO, Makoto  
; TITLE OF INVENTION: SOLUBLE HUMAN PROLACTIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/806,597A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/012,503  
; FILING DATE: 29 February 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: KELLY-1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 134 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-806-597A-8  
  
Query Match 58.2%; Score 679; DB 3; Length 134;  
Best Local Similarity 96.9%; Pred. No. 1.4e-65;  
Matches 125; Conservative 0; Mismatches 0; Indels 4; Gaps 2;  
  
QY 1 MKENVASATVFTLLFLNTCLLNGQLPGKPEIFKCRSPNKTFTCWRRPGTDGGLPTNY 60  
Db 1 MKENVASATVFTLLFLNTCLLNGQLPGKPEIFKCRSPNKTFTCWRRPGTDGGLPTNY 60  
  
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELVD 119  
Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELVD 120  
  
QY 120 VTYIVQPPD 128  
Db 121 VTYIVQPPD 126

RESULT 7  
US-08-970-428A-8  
; Sequence 8, Application US/08970428A  
; Patent No. 6083753  
; GENERAL INFORMATION:  
; APPLICANT: KELLY, Paul A. and NAGANO, Makoto  
; TITLE OF INVENTION: SOLUBLE HUMAN PROLACTIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970,428A  
FILING DATE: 14-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/012,503  
FILING DATE: 29-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/806,597  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: KELLY=1B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 134 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-970-428A-8

Query Match 58.2%; Score 679; DB 3; Length 134;  
Best Local Similarity 96.9%; Pred. No. 1.4e-65;  
Matches 125; Conservative 0; Mismatches 0; Indels 4; Gaps 2;  
QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
QY 61 SLTYHREGTLMHECPDYITGGNSCHFGKQYTSMTWRTYIMVNAT-QMGSSFSDELVD 119  
DB 61 SLTYHREGTLMHECPDYITGGNSCHFGKQYTSMTWRTYIMVNATQMGSSFSDELVD 120  
QY 120 VTYVQDPD 128  
DB 121 VTYI---DP 126

RESULT 8  
US-08-806-597A-4  
Sequence 4, Application US/08806597A  
Patent No. 6083714  
GENERAL INFORMATION:  
APPLICANT: KELLY, Paul A. and NAGANO, Makoto  
TITLE OF INVENTION: SOLUBLE HUMAN PROLACTIN RECEPTORS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/806,597A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/012,503

FILING DATE: 29 February 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KELLY=1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-806-597A-4

Query Match 33.2%; Score 387; DB 3; Length 118;  
Best Local Similarity 95.8%; Pred. No. 3.8e-34;  
Matches 69; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
QY 61 SLTYHREGTLM 72  
DB 61 SLTYHREGSILL 72

RESULT 9  
US-08-970-428A-4  
Sequence 4, Application US/08970428A  
Patent No. 6083753  
GENERAL INFORMATION:  
APPLICANT: KELLY, Paul A. and NAGANO, Makoto  
TITLE OF INVENTION: SOLUBLE HUMAN PROLACTIN RECEPTORS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/970,428A  
FILING DATE: 14-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/012,503  
FILING DATE: 29-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/806,597  
FILING DATE: 26-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: KELLY=1B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-970-428A-4

Query Match	33.2%; Score 387; DB 3; Length 118;	
Best Local Similarity	95.8%; Pred. No. 3.8e-34;	
Matches	69; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
QY	1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTFCWRPPTDGGGLPTNY 60	
Db	1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTFCWRPPTDGGGLPTNY 60	
QY	61 SLTYHREGETLM 72	
Db	61 SLTYHREGSILL 72	
RESULT 10		
US-09-071-224-25		
Sequence 25, Application US/09071224		
Patent No. 6271343		
GENERAL INFORMATION:		
APPLICANT: Lok, Si		
APPLICANT: Presnell, Scott R.		
APPLICANT: Jelmeberg, Anna C.		
APPLICANT: Gilbert, Teresa		
APPLICANT: Foster, Donald C.		
APPLICANT: Adams, Robyn L.		
APPLICANT: Lehner, Joyce M.		
TITLE OF INVENTION: MAMMALIAN ZCYTORS		
NUMBER OF SEQUENCES: 37		
CORRESPONDENCE ADDRESS:		
ADDRESSEE: Zymogenetics		
STREET: 1201 Eastlake Ave East		
CITY: Seattle		
STATE: WA		
COUNTRY: USA		
ZIP: 98102		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Diskette		
COMPUTER: IBM Compatible		
OPERATING SYSTEM: DOS		
SOFTWARE: FastSeq for Windows Version 2.0		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US/09/071.224		
FILING DATE:		
CLASSIFICATION:		
PRIOR APPLICATION DATA:		
APPLICATION NUMBER:		
FILING DATE:		
ATTORNEY/AGENT INFORMATION:		
NAME: Lunn, Paul G		
REGISTRATION NUMBER: 32,743		
REFERENCE/DOCKET NUMBER: 96-22		
TELECOMMUNICATION INFORMATION:		
TELEPHONE: 206-442-6627		
TELEFAX: 206-442-6678		
TELEX:		
INFORMATION FOR SEQ ID NO: 25:		
SEQUENCE CHARACTERISTICS:		
LENGTH: 389 amino acids		
TYPE: amino acid		
STRANDEDNESS: single		
TOPOLOGY: linear		
MOLECULE TYPE: protein		
US-09-071-224-25		
Query Match	25.5%; Score 297; DB 3; Length 389;	
Best Local Similarity	38.0%; Pred. No. 1.1e-23;	
Matches	76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;	
QY	15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTFCWRPPTDGG--LFTNYSLTYHREGETLM 72	
Db	86 ILAGSCLVVG-LPPEKPNVISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQGD 144	
QY	73 HECPDYITGGNSCHFGKQYTSWRYIMVNAT-QMGSSFSDELYVDVTVIVQDPDPLE 131	

Db	145 NTCEDYHTVGPHSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDLDVVTDDPPD 203
QY	132 LAV-EVKQPEDRKPYLWKWSPPTLIDLTGWTFTLLYEIRLKPKEAAEWE-IHFAGQOTE 189
Db	204 VHVSRVSGLEQLSVRWV--SPPALKDF---LFOAKYQIRYRVEDSVDMKVDDVDSNQT 258
QY	190 FKILSLHPGQXLYVVRCKP 209
Db	259 CRLAGLRPGTVYFVQVRCNP 278
RESULT 11	
US-09-071-224-26	
Sequence 26, Application US/09071224	
Patent No. 6271343	
GENERAL INFORMATION:	
APPLICANT: Lok, Si	
APPLICANT: Presnell, Scott R.	
APPLICANT: Jelmeberg, Anna C.	
APPLICANT: Gilbert, Teresa	
APPLICANT: Foster, Donald C.	
APPLICANT: Adams, Robyn L.	
APPLICANT: Lehner, Joyce M.	
TITLE OF INVENTION: MAMMALIAN ZCYTORS	
NUMBER OF SEQUENCES: 37	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: Zymogenetics	
STREET: 1201 Eastlake Ave East	
CITY: Seattle	
STATE: WA	
COUNTRY: USA	
ZIP: 98102	
COMPUTER READABLE FORM:	
MEDIUM TYPE: Diskette	
COMPUTER: IBM Compatible	
OPERATING SYSTEM: DOS	
SOFTWARE: FastSeq for Windows Version 2.0	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/09/071.224	
FILING DATE:	
CLASSIFICATION:	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	
FILING DATE:	
ATTORNEY/AGENT INFORMATION:	
NAME: Lunn, Paul G	
REGISTRATION NUMBER: 32,743	
REFERENCE/DOCKET NUMBER: 96-22	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: 206-442-6627	
TELEFAX: 206-442-6678	
TELEX:	
INFORMATION FOR SEQ ID NO: 26:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 389 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: protein	
US-09-071-224-26	
Query Match	25.5%; Score 297; DB 3; Length 389;
Best Local Similarity	38.0%; Pred. No. 1.1e-23;
Matches	76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;
QY	15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTFCWRPPTDGG--LFTNYSLTYHREGETLM 72
Db	86 ILAGSCLVVG-LPPEKPNVISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQGD 144
QY	73 HECPDYITGGNSCHFGKQYTSWRYIMVNAT-QMGSSFSDELYVDVTVIVQDPDPLE 131
Db	145 NTCEDYHTVGPHSCHIPKDLT-LFTPYEIVWEATNRLGARSVDLTLDLDVVTDDPPD 203

Query Match	25.4%	Score 296;	DB 3;	Length 303;
Best Local Similarity	38.0%	Pred. No. 9.5e-24;		
Matches	76;	Conservative	27;	Mismatches 85; Indels 12; Gaps 8;
xy	15	LFNTICLLNQLPKPGKFEIFKCRSPNKEFTCWWRPGTDGG-	LFNTNSLYLHREGETLM	72
bb	86	ILAGSCLYVG-LFPERPVNISCSWKMKDLTCRTWTFGAHGETFLHTNSLYLKYLRWVGQD	144	
xy	73	HECPDITGGPNSCHFGKQYTSWRITYIMNNAT-QMGSSPSDELYVDVTIVVDPDPPLE	131	
bb	145	NTCEEYHTVGPHSCHIPKO-LALFTFYEWVEATNRLGASRSDVLTLLILDVVTITDPPPE	203	
xy	132	LAV-EVKQPEDRKPYLWIKWSPPITLDLTGTFYLLYRILRKPKEAAEWI-IHFAGQOTE	189	

[illegible]

QY 190 FKILSLHPGQKYLQVRCRP 209  
 Db 259 CRLAGLKPQTVYFVQVRCNP 278

RESULT 14  
 US-09-071-224-17  
 ; Sequence 17, Application US/09071224  
 ; Patent No. 6271343  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lok, Si  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: Jelmsberg, Anna C.  
 ; APPLICANT: Gilbert, Teresa  
 ; APPLICANT: Foster, Donald C.  
 ; APPLICANT: Adams, Robyn L.  
 ; APPLICANT: Lehner, Joyce M.  
 ; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Zymogenetics  
 ; STREET: 1201 Eastlake Ave East  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/071,224  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lunn, Paul G  
 ; REGISTRATION NUMBER: 32,743  
 ; REFERENCE/DOCKET NUMBER: 96-22  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 206-442-6627  
 ; TELEFAX: 206-442-6678  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 17:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 388 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-071-224-17

Query Match 25.4%; Score 296; DB 3; Length 388;  
 Best Local Similarity 38.0%; Pred. No. 1.3e-23;  
 Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;  
 QY 15 LFLNLTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTYYHREGTLM 72  
 Db 89 ILAGSLYVG-LPPEKPNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQD 147  
 QY 73 HECPDYITGGNSCHFGKQYTSNWRTYIMVNAT-OMGSSFSDELYVDVTYIVQDPPE 131  
 Db 148 NTCSEYHTVGPCHSHPKD-LALFTPEYIWEATNRLGSRSDVLTLDLDVVTDDPPPE 206  
 QY 132 LAV-EVKQPEDRKPYLWIKWSPTLIDLTGFTLLYEIRLKPKEAAWE-IHFAGQOTE 189  
 Db 207 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVSDSVDMKVVDDVSNQTS 261  
 QY 190 FKILSLHPGQKYLQVRCRP 209

Db 262 CRLAGLKPQTVYFVQVRCNP 281  
 RESULT 15  
 US-09-071-224-27  
 ; Sequence 27, Application US/09071224  
 ; Patent No. 6271343  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lok, Si  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: Jelmsberg, Anna C.  
 ; APPLICANT: Gilbert, Teresa  
 ; APPLICANT: Foster, Donald C.  
 ; APPLICANT: Adams, Robyn L.  
 ; APPLICANT: Lehner, Joyce M.  
 ; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Zymogenetics  
 ; STREET: 1201 Eastlake Ave East  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/071,224  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lunn, Paul G  
 ; REGISTRATION NUMBER: 32,743  
 ; REFERENCE/DOCKET NUMBER: 96-22  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 206-442-6627  
 ; TELEFAX: 206-442-6678  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 27:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 399 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-071-224-27

Query Match 25.4%; Score 296; DB 3; Length 389;  
 Best Local Similarity 38.0%; Pred. No. 1.3e-23;  
 Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;  
 QY 15 LFLNLTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTYYHREGTLM 72  
 Db 86 ILAGSLYVG-LPPEKPNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQD 144  
 QY 73 HECPDYITGGNSCHFGKQYTSNWRTYIMVNAT-OMGSSFSDELYVDVTYIVQDPPE 131  
 Db 145 NTCSEYHTVGPCHSHPKD-LALFTPEYIWEATNRLGSRSDVLTLDLDVVTDDPPPD 203  
 QY 132 LAV-EVKQPEDRKPYLWIKWSPTLIDLTGFTLLYEIRLKPKEAAWE-IHFAGQOTE 189  
 Db 204 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVSDSVDMKVVDDVSNQTS 258  
 QY 190 FKILSLHPGQKYLQVRCRP 209  
 Db 259 CRLAGLKPQTVYFVQVRCNP 278

Thu May 13 08:55:52 2004

us-10-029-079-3.ra1

Page 8

Search completed: May 12, 2004, 16:20:03  
Job time : 23 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:10:55 ; Search time 61 Seconds  
(without alignments)  
972.705 Million cell updates/sec

Title: US-10-029-079-3  
Perfect score: 1166  
Sequence: 1 MKENVASATVFTLLFLNTC.....KILSLHPGQKYLQVRCKPD 210

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1166	100.0	210	5	Abg70827 Human rec
2	1155.5	99.1	349	3	Aay96921 Soluble h
3	1155.5	99.1	349	3	Aay95527 Human pro
4	1155.5	99.1	622	2	Aar10795 Human pro
5	1155.5	99.1	622	5	Abj05555 Breast ca
6	1155.5	99.1	622	5	Aau99354 Human pro
7	1155.5	99.1	622	6	Abr47567 Breast ca
8	1154.5	99.0	622	5	Aau99355 Human pro
9	1036.5	88.9	211	2	Aar24273 Truncated
10	1036.5	88.9	211	2	Aar22228 Truncated
11	987	84.6	597	7	Ade28697 Human NOV
12	679	58.2	134	3	Aay96918 Soluble h
13	679	58.2	134	3	Aay95526 Soluble i
14	549.5	47.1	606	2	Aar93121 Tilapia p
15	549.5	47.1	630	2	Aar93120 Tilapia p
16	387	33.2	118	3	Aay96916 Soluble h
17	387	33.2	118	3	Aay95524 Soluble i
18	297	25.5	389	2	Aaw70847 Human zcy
19	297	25.5	389	2	Aaw70848 Human zcy
20	296	25.4	303	2	Aaw70843 Human zcy
21	296	25.4	385	2	Aaw70842 Human zcy
22	296	25.4	388	2	Aaw70839 Human zcy
23	296	25.4	389	2	Aaw70849 Human zcy
24	296	25.4	389	2	Aaw70853 Human zcy
25	296	25.4	422	2	Aaw70860 Human zcy

26	295	25.3	183	2	Aar25244	Truncated
27	295	25.3	389	2	Aaw70852	Human zcy
28	294	25.2	389	2	Aaw70851	Human zcy
29	294	25.2	389	2	Aaw70846	Human zcy
30	294	25.2	389	2	Aaw70850	Human zcy
31	293	25.1	303	2	Aaw70845	Human zcy
32	293	25.1	350	2	Aaw55015	Amino aci
33	293	25.1	350	4	Aae00824	Human NR6
34	293	25.1	389	2	Aaw70844	Human zcy
35	293	25.1	392	2	Aaw70840	Human zcy
36	293	25.1	408	2	Aaw59805	Amino aci
37	293	25.1	408	2	Aay26338	Human U4
38	293	25.1	410	2	Aay29779	Human DNA
39	293	25.1	410	3	Aab19588	Human cyt
40	293	25.1	410	4	Aab36647	Human cyt
41	293	25.1	410	7	Adc07179	Human cyt
42	293	25.1	421	4	Aae00826	Murine ha
43	293	25.1	422	2	Aay05782	Human typ
44	293	25.1	422	2	Aay06479	Human tum
45	293	25.1	422	2	Aay17825	Human PRO

ALIGNMENTS

RESULT 1

ABG70827  
ID ABG70827 standard; protein; 210 AA.  
XX  
AC ABG70827;  
XX  
DT 17-DEC-2002 (first entry)  
XX  
DE Human recombinant prolactin-binding protein, rhPRLBP.  
XX  
KW Human; prolactin-binding protein; PRLBP; prolactin receptor; PRLR;  
KW growth hormone receptor; GHR; transmembrane protein; hormone; prolactin;  
KW PRL; growth hormone; GH; homodimerisation; receptor-associated kinase;  
KW signalling cascade; rhPRLBP; recombinant hPRLBP; extracellular domain;  
KW ECD; cancer; Nb2; cellular proliferation; diagnosis; somatolactogenic;  
KW pituitary adenoma; hyperprolactinaemia; gigantism; acromegaly;  
KW osteopathic.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 106..107  
FT /note= "Encoded by ACTAACCAG"  
XX  
XX US2002119154-A1.  
XX  
XX 29-AUG-2002.  
XX  
XX 21-DEC-2001; 2001US-00029079.  
XX  
XX 22-DEC-2000; 2000US-0258285P.  
XX  
XX (CLEV/) CLEVENGER C V.  
XX (KLIN/) KLINE J B.  
XX  
XX Clevenger CV, Kline JB;  
XX WPI: 2002-750044/81.  
XX N-PSDB; ABS55241.  
XX  
XX Novel human prolactin-binding protein, useful for modulating  
XX somatolactogenic function and for inhibiting Nb2 cells in animals.  
XX  
XX Disclosure; Page 6; 13pp; English.  
XX  
XX The invention discloses a human prolactin-binding protein (PRLBP). Both  
XX the prolactin receptor (PRLR) and the growth hormone receptor (GHR) are  
XX single chain transmembrane proteins. The hormones prolactin (PRL) and



```

XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Kelly PA, Nagano M;
XX
DR WPI; 2000-464346/40.
DR N-PSDB; AAA49980.
XX
XX New recombinant DNA having a segment encoding a signal peptide joined
PT translationally to a segment encoding a soluble human prolactin receptor
PT useful as a hormone growth hormone binding protein, and in x-ray
PT crystallographic analysis.
XX
XX Claim 15; Col 35-38; 27pp; English.
XX
XX The present sequence is that of a newly identified isoform of the human
CC prolactin receptor (PRLR), which lacks a large part of the intracellular
CC domain (amino acids 312-503) of the full-length receptor and has a short
CC cytoplasmic tail. 6 isoforms (see AAA49976-82) of human PRLR have been
CC identified in human colonic Caco-2 and human breast cancer T-47D cells.
CC Recombinant DNA molecules encoding the soluble PRLR proteins are
CC provided, as well as expression vectors and host cells. The soluble PRLRs
CC may be used as binding proteins for human prolactin and/or human growth
CC hormone, which can be useful in diagnostics for the detection and
CC measurement of the binding ligand, or in therapeutics for binding to
CC human prolactin and/or human growth hormone to retard or inhibit their
CC hormone activities. They may also be used in place of monoclonal
CC antibodies to provide solution-based radioligand receptor assays, in
CC receptor sandwich or enzymatic assays, and in x-ray crystallographic
CC analysis to develop molecular models that define the tertiary structure
CC of the hormone-binding domains, where such information would provide
CC insight into the structure of the actual contact between a hormone and
CC its receptor. This structural information would be useful in the design
CC of peptides that have prolactin or growth hormone-like agonistic or
CC antagonistic activity
XX
XX Sequence 349 AA;
XX
XX Query Match 99.1%; Score 1155.5; DB 3; Length 349;
XX Best Local Similarity 99.5%; Pred. No. 1.4e-105;
XX Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGLPTNY 60
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMMRTYIMMNVNAT-OMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMMRTYIMMNVNAT-OMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPAAEW 179
DB 121 VTYIVQDPDPLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPAAEW 180
QY 180 EIHPAGQQTTEFKILSLHFGQKYLQVVRCKPD 210
DB 181 EIHPAGQQTTEFKILSLHFGQKYLQVVRCKPD 211
XX
XX RESULT 4
XX ID AAR10795 standard; protein; 622 AA.
XX AC AAR10795;
XX DT 25-APR-1991 (first entry)
XX XX Human prolactin receptor.
XX DE Human prolactin receptor.
XX KW Human prolactin receptor; PRL; assay; antibody; growth hormone.
XX XX Homo sapiens.
XX OS

```

```

XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= sig_peptide
FT Protein 25..622
FT /label= mat_protein
XX
XX US4992378-A.
XX
XX 12-FEB-1991.
XX
XX 16-DEC-1988; 88US-00286445.
XX
XX 16-DEC-1988; 88US-00286445.
XX
XX (ROYA-) ROYAL INST ADVAN LE.
XX
XX Kelly PA, Djiane J;
XX
XX WPI; 1991-065341/09.
XX N-PSDB; AAQ10550.
XX
XX Isolated cDNA sequence encoding human prolactin receptor - useful for
XX expressing the receptor, e.g. for screening assays and antibody prodn.
XX
XX Disclosure; Fig 1 (A-E); 11pp; English.
XX
XX The human PRL receptor cDNA is isolated by screening a lambda gt 10
XX library prepared from normal human hepatoma Hep G2 and T47-D breast
XX cancer cells. Initially, 1x106 recombinants are screened with the
XX following probe: a complementary RNA of the F3 cDNA of the rat prolactin
XX receptor. One positive recombinant was isolated from the Hep G2 library;
XX cDNA was later used as a probe to rescreen the library. Five additional
XX cDNAs were identified, and by combining two of the six cDNAs, a PRL
XX receptor cDNA of 2.5 kb was constructed, contg. a single ORF of 1866 bp.
XX Similar partial length cDNA were isolated from the T47-D library. Several
XX regions of sequence identity between the human growth hormone and PRL
XX receptors can be found, both in the extracellular and cytoplasmic
XX domains. The sequence is an important genetic engineering tool which may
XX be used for the screening of growth hormone variants, for the development
XX of test kits to measure PRL receptor levels in human breast and prostate
XX cancer biopsies, for the measurement of bioactive forms of prolactin,
XX and for the development of drugs to induce stimulation or inhibition of
XX the immune system
XX
XX Sequence 622 AA;
XX
XX Query Match 99.1%; Score 1155.5; DB 2; Length 622;
XX Best Local Similarity 99.5%; Pred. No. 2.9e-105;
XX Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGLPTNY 60
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMMRTYIMMNVNAT-OMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMMRTYIMMNVNAT-OMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPAAEW 179
DB 121 VTYIVQDPDPLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPAAEW 180
QY 180 EIHPAGQQTTEFKILSLHFGQKYLQVVRCKPD 210
DB 181 EIHPAGQQTTEFKILSLHFGQKYLQVVRCKPD 211
XX
XX RESULT 5
XX ABJ05555
XX ID ABJ05555 standard; protein; 622 AA.
XX XX
XX AC ABJ05555;

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XX  
DT 14-NOV-2002 (first entry)  
XX  
DE Breast cancer-associated protein 20.  
XX  
KW Breast cancer; breast cancer-associated gene sequence; drug development;  
KW pharmacogenetics; biosensor development.  
XX  
OS Unidentified.  
XX  
PN W0200259377-A2.  
XX  
PD 01-AUG-2002.  
XX  
XX 24-JAN-2002; 2002WO-US002242.  
XX  
XX 24-FEB-2001; 2001US-0263965P.  
XX  
PR 02-FEB-2001; 2001US-0265928P.  
XX  
PR 09-APR-2001; 2001US-00829472.  
XX  
PR 09-APR-2001; 2001US-0282698P.  
XX  
PR 04-MAY-2001; 2001US-0288590P.  
XX  
PR 29-MAY-2001; 2001US-0294443P.  
XX  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
XX Mack DH, Gish KC, Afar D;  
XX  
XX WPI; 2002-583738/62.  
XX  
DR N-PSDB; ABT07712.  
XX  
XX Detecting a breast cancer-associated transcript in a patient's cell.  
XX  
PT useful for diagnosing breast cancer, comprises contacting a biological  
PT sample with a polynucleotide that selectively hybridizes with breast  
PT cancer nucleic acids.  
XX  
XX Disclosure; Page 365; 414pp; English.  
XX  
PS The invention comprises a method of detecting a breast cancer-associated  
PS transcript in a cell from a patient. The method of the invention involves  
CC contacting a biological sample from the patient with a nucleotide that  
CC hybridizes to one of the 69 breast cancer-associated gene sequences shown  
CC in the specification. The method of the invention is useful in the  
CC diagnosis or prognosis of breast cancer, and for detecting genes that are  
CC up or down-regulated in breast cancer cells. Genes identified by the  
CC method of the invention can be used in diagnostic purposes and also as  
CC targets for screening for therapeutic compounds that modulate breast  
CC cancer (e.g. hormones or antibodies). Identification of genes that are  
CC over or under expressed in breast cancer can additionally provide high-  
CC resolution, high-sensitivity datasets which can be used in the areas of  
CC diagnostics, therapeutics, drug development, pharmacogenetics, protein  
CC structure and biosensor development. Amino acid sequences ABJ05536 -  
CC ABJ05604 represent the proteins encoded by the 69 breast cancer-  
CC associated genes of the invention  
XX  
XX Sequence 622 AA;  
XX  
Query Match 99.1%; Score 1155.5; DB 5; Length 622;  
Best Local Similarity 99.5%; Pred. No. 2.9e-105;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MKENVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
DB 1 MKENVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQVTSWRTYIMVNAT-QWGSFSFSDLYVD 119  
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQVTSWRTYIMVNATQWGSFSFSDLYVD 120  
QY 120 VYIYVQDPDPLELAVEVKQPEDRKPYLWIKWSPFLIDIKTGWFTLLYEIRLKPKEAEW 179  
DB 121 VYIYVQDPDPLELAVEVKQPEDRKPYLWIKWSPFLIDIKTGWFTLLYEIRLKPKEAEW 180  
QY 180 EHFAGQQTFFKILSLHPGQKYLVOVRCKPD 210

DB 181 EHFAGQQTFFKILSLHPGQKYLVOVRCKPD 211  
RESULT 6  
AAU99354  
ID AAU99354 standard; protein; 622 AA.  
XX  
AC AAU99354;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
XX Human prolactin receptor (PRLR) protein.  
XX  
XX Human; receptor; prolactin receptor; PRLR; cytostatic; immunosuppressive;  
KW chromosome 5p14-p13; neuroendocrine hormone; prolactin; PRL;  
KW breast growth; breast differentiation; puberty; pregnancy; lactation;  
KW mammary disorder; breast cancer; autoimmune disease; hyperprolactinaemia;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
XX W0200250098-A2.  
XX  
XX 27-JUN-2002.  
XX  
XX 18-DEC-2001; 2001WO-US049049.  
XX  
XX 18-DEC-2000; 2000US-0256523P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
XX  
XX Bieglecki KM, Duda A, Koshy B;  
XX  
XX WPI; 2002-528446/56.  
XX  
XX N-PSDB; ABK87971.  
XX  
XX Novel genetic variants of Prolactin Receptor isogenes, useful for  
XX improving efficiency and reliability in drug development for treating  
XX breast cancer, autoimmune diseases and hyperprolactinemia.  
XX  
XX Claim 27; Fig 3; 81pp; English.  
XX  
XX The invention discloses an isolated polynucleotide and polypeptide of the  
XX human prolactin receptor (PRLR). The neuroendocrine hormone prolactin  
XX (PRL) stimulates breast growth and differentiation during puberty,  
XX pregnancy and lactation. PRL has been implicated in the etiology of  
XX mammary disorders, such as breast cancer, and since PRLR mediates the  
XX effects of prolactin, it may also be involved in the etiology of the  
XX disease. The polypeptides are useful in screening for drugs that are  
XX useful for treating breast cancer, autoimmune diseases,  
XX hyperprolactinaemia and diseases associated with PRLR activity. The  
XX haplotyping method is also used by the pharmaceutical research scientist  
XX to validate PRLR as a candidate target for treating these specific  
XX conditions or diseases predicted and in the design of clinical trials for  
XX treating a specific condition of disease associated with PRLR activity.  
XX Antibodies raised against PRLR are useful in diagnostic, prognostic and  
XX therapeutic methods. The polynucleotide is useful for gene therapy and in  
XX studying the expression and function of PRLR and the effect of the single  
XX nucleotide polymorphisms (SNP) on the biological activity of PRLR. The  
XX sequence presented is the human prolactin receptor (PRLR) protein which  
XX is encoded by the gene located on chromosome 5p.4-p13  
XX  
XX Sequence 622 AA;  
XX  
Query Match 99.1%; Score 1155.5; DB 5; Length 622;  
Best Local Similarity 99.5%; Pred. No. 2.9e-105;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MKENVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
DB 1 MKENVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60

```
QY 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSWRTYIMMWNAT-QMGSSFSDELYVD 119
Db 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSWRTYIMMWNATQMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLELAVEVKQPEDRKPYLWIKWSPPTLIDLTGFTLLYIIRLKPEKAAEW 179
Db 121 VTYIVQDPDPLELAVEVKQPEDRKPYLWIKWSPPTLIDLTGFTLLYIIRLKPEKAAEW 180
QY 180 EIHFAQQTEFKILSLHPGQKYLIVQVRCKPD 210
Db 181 EIHFAQQTEFKILSLHPGQKYLIVQVRCKPD 211

RESULT 7
ABR47567
ID ABR47567 standard; protein; 622 AA.
AC
XX ABR47567;
XX
DT 12-JUN-2003 (first entry)
XX
DE Breast cancer associated protein sequence SEQ ID NO:373.
XX
KW Human; breast cancer; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003004989-A2.
XX
PD 16-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019669.
XX
PR 21-JUN-2001; 2001US-0299987P.
XX
PR 27-JUN-2001; 2001US-0301572P.
XX
PR 18-JUL-2001; 2001US-0306501P.
XX
PR 25-SEP-2001; 2001US-0325002P.
XX
PR 05-MAR-2002; 2002US-0362585P.
XX
PR 14-MAY-2002; 2002US-0380391P.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;
XX
WPI: 2003-210381/20.
DR N-PSDB; ACC50266.
XX
Breast cancer diagnosis or treatment by comparing the level of expression
of a marker in a patient sample with that in the control non-breast
cancer sample.
XX
Claim 1; SEQ ID NO 373; 128pp; English.
XX
The present invention describes a method for assessing whether a patient
is afflicted with breast cancer. The method comprises comparing the level
of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
ABR47386 to ABR47632) in a patient sample and the normal level of
expression of the marker in a control non-breast cancer sample, where a
significant increase in the level of expression of the marker in the
patient sample and the normal level is an indication that the patient is
afflicted with breast cancer. The breast cancer associated sequences from
the present invention have cytostatic activities and can be used in gene
therapy. The method is useful for diagnosing and treating breast cancer.
N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences
XX
SQ Sequence 622 AA;
Query Match 99.1%; Score 1155.5; DB 6; Length 622;
Best Local Similarity 99.5%; Pred. No. 2.9e-105;
```

```
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MKENVASATVFTLLFLNLTCLNGQLPPGKPEIFKCRSPNKETTCWWRPGTDGGLPTNY 60
Db 1 MKENVASATVFTLLFLNLTCLNGQLPPGKPEIFKCRSPNKETTCWWRPGTDGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSWRTYIMMWNAT-QMGSSFSDELYVD 119
Db 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSWRTYIMMWNATQMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLELAVEVKQPEDRKPYLWIKWSPPTLIDLTGFTLLYIIRLKPEKAAEW 179
Db 121 VTYIVQDPDPLELAVEVKQPEDRKPYLWIKWSPPTLIDLTGFTLLYIIRLKPEKAAEW 180
QY 180 EIHFAQQTEFKILSLHPGQKYLIVQVRCKPD 210
Db 181 EIHFAQQTEFKILSLHPGQKYLIVQVRCKPD 211

RESULT 8
AAU99355
ID AAU99355 standard; protein; 622 AA.
XX
AC AAU99355;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human prolactin receptor (PRLR) variant protein.
XX
KW Human; receptor; prolactin receptor; PRLR; cytostatic; immunosuppressive;
KW chromosome 5p14-p13; neuroendocrine hormone; prolactin; PRL;
KW breast growth; breast differentiation; puberty; pregnancy; lactation;
KW mammary disorder; breast cancer; autoimmune disease; hyperprolactinaemia;
KW gene therapy; single nucleotide polymorphism; SNP.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 100
ET /note= "Ile substituted by Val"
XX
WO200250099-A2.
XX
PD 27-JUN-2002.
XX
PF 18-DEC-2001; 2001WO-US049049.
XX
PR 18-DEC-2000; 2000US-0256523P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bieglecki KM, Duda A, Koshiy B;
XX
WPI: 2002-528446/56.
DR N-PSDB; ASK87971.
XX
Novel genetic variants of Prolactin Receptor isogenes, useful for
improving efficiency and reliability in drug development for treating
breast cancer, autoimmune diseases and hyperprolactinemia.
XX
Claim 27; Page; 81pp; English.
XX
The invention discloses an isolated polynucleotide and polypeptide of the
human prolactin receptor (PRLR). The neuroendocrine hormone prolactin
(PRL) stimulates breast growth and differentiation during puberty,
pregnancy and lactation. PRL has been implicated in the etiology of
mammary disorders, such as breast cancer, and since PRLR mediates the
effects of prolactin, it may also be involved in the etiology of the
disease. The polypeptides are useful in screening for drugs that are
useful for treating breast cancer, autoimmune diseases,
hyperprolactinaemia and diseases associated with PRLR activity. The
hplotyping method is also used by the pharmaceutical research scientist
to validate PRLR as a candidate target for treating these specific
```

CC conditions or diseases predicted and in the design of clinical trials for  
 CC treating a specific condition of disease associated with PRLR activity.  
 CC Antibodies raised against PRLR are useful in diagnostic, prognostic and  
 CC therapeutic methods. The polynucleotide is useful for gene therapy and in  
 CC studying the expression and function of PRLR and the effect of the single  
 CC nucleotide polymorphisms (SNP) on the biological activity of PRLR. The  
 CC sequence presented is the human prolactin receptor (PRLR) protein,  
 CC variant #2, which is encoded by the gene located on chromosome 3p14-p13.  
 CC Note: This sequence is not shown in the specification but was created by  
 CC the indexer from information given in figure 3

XX SQ Sequence 622 AA;

Query Match 99.0%; Score 1154.5; DB 5; Length 622;  
 Best Local Similarity 99.1%; Pred. No. 3.6e-105;  
 Matches 209; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60  
 DB 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60  
 QY 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMWRTYIMVNAT-QMGSSFSDELYVD 119  
 DB 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMWRTYIMVNATQMGSSFSDELYVD 120  
 QY 120 VTYIVQDPPLLELAVEVKQPEDSKPYLWIKWSPPTLIDLTGWTLLYELRLKPEKAAEW 179  
 DB 121 VTYIVQDPPLLELAVEVKQPEDSKPYLWIKWSPPTLIDLTGWTLLYELRLKPEKAAEW 180  
 QY 180 EHFAGQQTFFKLSLHPGQKYLIVQVRCRPD 210  
 DB 181 EHFAGQQTFFKLSLHPGQKYLIVQVRCRPD 211

RESULT 9

AAR24273  
 ID AAR24273 standard; protein; 211 AA.

XX AC AAR24273;

XX DT 20-JUL-1992 (first entry)

XX DE Truncated human prolactin binding protein variant.

XX KW hPRLbp; placental lactogen; zinc finger; chelate;  
 XX KW receptor-ligand complex.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 188 /note= "wild-type His replaced by Ala"

XX PN WO9203478-A.

XX PD 05-MAR-1992.

XX PF 16-AUG-1991; 91WO-US005856.

XX PR 17-AUG-1990; 90US-00568936.

XX PA (GETH ) GENENTECH INC.

XX PI Bass SH, Cunningham BC, Fuh G, Lowman HB, Matthews DJ, Wells JA;

XX DR WPI; 1992-096838/12.

XX PT New method of modifying polypeptide hormone-receptor complex - to produce  
 XX PT human growth hormone variant, useful for stimulating lactogenic and  
 XX PT somatogenic response.

XX PS Claim 41; Page 56; 74pp; English.

XX XX

CC Plasmid pHPRLbp(1-211) (see AAR22228) coding for truncated, soluble  
 CC prolactin binding protein was mutagenised such that the His codon at  
 CC position 188 was substituted by an Ala codon. The hPRLbp variant has  
 CC altered binding affinity for hGH

XX SQ Sequence 211 AA;

Query Match 88.9%; Score 1036.5; DB 2; Length 211;  
 Best Local Similarity 99.5%; Pred. No. 4.3e-94;  
 Matches 186; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 25 QLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTVHREGETLMHECPDYITGGPN 84  
 DB 1 QLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTVHREGETLMHECPDYITGGPN 60  
 QY 85 SCHFGKQYTSMWRTYIMVNAT-QMGSSFSDELYVDVTYIVQDPPLLELAVEVKQPEDRK 143  
 DB 61 SCHFGKQYTSMWRTYIMVNATQMGSSFSDELYVDVTYIVQDPPLLELAVEVKQPEDRK 120  
 QY 144 PYLWIKWSPPTLIDLTGWTLLYELRLKPEKAAEWIHFAGQQTFFKLSLHPGQKYLIV 203  
 DB 121 PYLWIKWSPPTLIDLTGWTLLYELRLKPEKAAEWIHFAGQQTFFKLSLHPGQKYLIV 180  
 QY 204 QVRCCKPD 210  
 DB 181 QVRCCKPD 187

RESULT 10

AAR22228  
 ID AAR22228 standard; protein; 211 AA.

XX AC AAR22228;

XX DT 20-JUL-1992 (first entry)

XX DE Truncated human prolactin binding protein.

XX KW hPRLbp; placental lactogen; zinc finger; chelate;  
 XX KW receptor-ligand complex.

XX OS Homo sapiens.

XX PN WO9203478-A.

XX PD 05-MAR-1992.

XX PF 16-AUG-1991; 91WO-US005856.

XX PR 17-AUG-1990; 90US-00568936.

XX PA (GETH ) GENENTECH INC.

XX PI Bass SH, Cunningham BC, Fuh G, Lowman HB, Matthews DJ, Wells JA;

XX DR WPI; 1992-096838/12.

XX PT New method of modifying polypeptide hormone-receptor complex - to produce  
 XX PT human growth hormone variant, useful for stimulating lactogenic and  
 XX PT somatogenic response.

XX PS Disclosure; Page 41; 74pp; English.

XX CC This truncated human prolactin binding protein is encoded by the insert  
 CC contained in plasmid pHPRLbp(1-211). The hPRLbp gene fragment is  
 CC transcribed under the control of the alkaline phosphatase promoter and  
 CC secreted into the host (E.coli) periplasm under the direction of the stII  
 CC signal sequence. A stop codon and MluI restriction site were introduced  
 CC after the threonine 211 codon which immediately precedes the  
 CC transmembrane domain of the receptor. The plasmid was used as a template  
 CC for site-directed mutagenesis to modify the metal-chelating centre of the  
 CC protein. See e.g. AAR24273 for an example of a preferred variant

SQ	Sequence 211 AA;	
Query Match	88.9%; Score 1036.5; DB 2; Length 211;	
Best Local Similarity	99.5%; Pred. No. 4.3e-94;	
Matches 186; Conservative	0; Mismatches 0; Indels 1; Gaps 1;	
QY	25 QLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNYSLTYHREGETLMHECPDYITGGPN 84	
DB	1 QLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNYSLTYHREGETLMHECPDYITGGPN 60	
QY	85 SCHFGKQYTSMWRTYIMVNAT-QMGSSFSDELYVDVTYIVQDPDPLELAVSVKQEDRK 143	
DB	61 SCHFGKQYTSMWRTYIMVNATQMGSSFSDELYVDVTYIVQDPDPLELAVSVKQEDRK 120	
QY	144 PYLWIKWSPPTLIDLKTGFTLLYEIRLKPKEAEWIEHFAGQOTBFKILSLHPGQKYLIV 203	
DB	121 PYLWIKWSPPTLIDLKTGFTLLYEIRLKPKEAEWIEHFAGQOTBFKILSLHPGQKYLIV 180	
QY	204 QVRCKPD 210	
DB	181 QVRCKPD 187	
RESULT 11		
ADE28697	ID ADE28697 standard; protein; 597 AA.	
XX	AC ADE28697;	
XX	29-JAN-2004 (first entry)	
DE	Human NOV18a protein - SEQ ID 74.	
XX	NOVX; antidiabetic; anorectic; cardiatic; hypotensive;	
KW	antiarteriosclerotic; virucide; antibacterial; fungicide; protozoacide;	
KW	nootropic; neuroprotective; antiparkinsonian; anticonvulsant;	
KW	osteopathic; antiarthritic; antiinflammatory; dermatological;	
KW	antiasthmatic; antilipemic; metabolic; diabetes; obesity; infectious;	
KW	anorexia; cancer; cardiovascular; hypertension; atherosclerosis;	
KW	neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune;	
KW	osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia;	
KW	neurogenesis; cell differentiation; proliferation; haemopoiesis;	
KW	wound healing; angiogenesis; gene therapy; chromosome mapping;	
KW	tissue typing; human; NOV.	
XX	Homo sapiens.	
XX	WO2003040330-A2.	
XX	15-MAY-2003.	
XX	05-NOV-2002; 2002WO-US035536.	
XX	05-NOV-2001; 2001US-0338626P.	
PR	05-DEC-2001; 2001US-0336600P.	
PR	07-DEC-2001; 2001US-0338285P.	
PR	12-DEC-2001; 2001US-0341346P.	
PR	17-DEC-2001; 2001US-0341477P.	
PR	17-DEC-2001; 2001US-0341540P.	
PR	20-DEC-2001; 2001US-0342592P.	
PR	27-DEC-2001; 2001US-0344237P.	
PR	31-DEC-2001; 2001US-0344903P.	
PR	17-APR-2002; 2002US-0373288P.	
PR	15-MAY-2002; 2002US-0380981P.	
PR	17-MAY-2002; 2002US-0381495P.	
PR	28-MAY-2002; 2002US-0383534P.	
PR	28-MAY-2002; 2002US-0383744P.	
PR	29-MAY-2002; 2002US-0383829P.	
PR	29-MAY-2002; 2002US-0384024P.	
PR	07-AUG-2002; 2002US-0401788P.	
PR	26-AUG-2002; 2002US-0406353P.	
PR	31-OCT-2002; 2002US-00287971.	
XX		
PA	(CURA-) CURAGEN CORP.	
XX	Alsbrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;	
PI	Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;	
PI	Ellerman K, Etenberg S, Gangoli EA, Gerlach VL, Gorman L;	
PI	Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khrantsov NV;	
PI	Lepley DM, Li L, Macougall JR, Malyankar UM, Mazur A, Mequenev K;	
PI	Mezes PS, Miller CE, Millet I, Mishra VS, Padigara M, Patturajan M;	
PI	Pena CBA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;	
PI	Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twonlow N;	
PI	Vernet CAM, Zerhusen BD, Zhong M;	
XX	WPI; 2003-441555/41.	
DR	N-PSDB; ADE28696.	
XX	New isolated NOVX polypeptides and polynucleotides, useful for	
PT	preventing, diagnosing or treating NOVX-associated disorders, e.g.	
PT	osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,	
PT	asthma, or infections.	
XX	Claim 1; SEQ ID NO 74; 447pp; English.	
XX	The invention relates to a novel isolated NOVX polypeptide. The	
CC	polypeptide of the invention demonstrates, antidiabetic, anorectic,	
CC	cardiac, hypotensive, antiarteriosclerotic, virucide, antibacterial,	
CC	fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonian,	
CC	anticonvulsant, osteopathic, antiarthritic, antiinflammatory,	
CC	dermatological, antiasthmatic and antilipemic activities. The	
CC	polypeptides, nucleic acid molecules and antibodies may be useful for	
CC	treating or diagnosing diseases including metabolic disorders such as	
CC	diabetes and obesity, infectious diseases, anorexia, cancer,	
CC	cardiovascular diseases including hypertension and atherosclerosis,	
CC	neurodegenerative disorders such as Alzheimer's disease, Parkinson's	
CC	disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic	
CC	disorders, inflammatory skin disorders, asthma and dyslipidaemia.	
CC	Furthermore, the nucleic acids and polypeptides may also be used to	
CC	identify molecules that modulate or inhibit neurogenesis, cell	
CC	differentiation and proliferation, haemopoiesis, wound healing and	
CC	angiogenesis, as well as in gene therapy. Finally, the nucleic acids may	
CC	be used as hybridisation probes, in chromosome mapping, tissue typing,	
CC	preventive medicine and pharmacogenomics. The current sequence is that of	
CC	the human NOV protein of the invention.	
XX	Sequence 597 AA;	
SQ	Query Match 84.6%; Score 987; DB 7; Length 597;	
	Best Local Similarity 87.7%; Pred No. 1.2e-88;	
	Matches 185; Conservative 0; Mismatches 0; Indels 26; Gaps 2;	
QY	1 MKENVASATVFTLLFLNTCLINGQLPFGKPEIFKCRSPNKETFTCWRRPGTDGGLP 60	
DB	1 MKENVASATVFTLLFLNTCLINGQLPFGKPEIFKCRSPNKETFTCWRRPGTDGGLP 58	
QY	61 SLTYHREGETLMHECPDYITGPNNSCHFGKQYTSMWRTYIMVNAT-QMGSSFSDELYVD 119	
DB	59 -----NSCHFGKQYTSMWRTYIMVNATQMGSSFSDELYVD 95	
QY	120 VTYIVQPPPLELAVEVKQPEDEKPYLWKSPPTLIDLKTGFTLLYEIRLKPKEAEW 179	
DB	96 VTYIVQPPPLELAVEVKQPEDEKPYLWKSPPTLIDLKTGFTLLYEIRLKPKEAEW 155	
QY	180 EHFAGQOTFEKILSLHPGQKYLIVQVRCKPD 210	
DB	156 EHFAGQOTFEKILSLHPGQKYLIVQVRCKPD 186	
RESULT 12		
ID	AA96918	
ID	AA96918 standard; protein; 134 AA.	
XX	AA96918;	
XX	AC AA96918;	
XX	31-OCT-2000 (first entry)	
DT		





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Db      1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNY 60
Qy      61 SLTYHREGELTHCECPDYITGGNSCHFGKQYTSMTTYIMVNAT-QMGSSFSDELYVD 119
Db      61 SLTYHREGELTHCECPDYITGGNSCHFGKQYTSMTTYIMVNATQMGSSFSDELYVD 120
Qy      120 VTYIVQDPD 128
Db      121 VTYI---DP 126

RESULT 14
AAR93121
ID AAR93121 standard; protein; 606 AA.
XX AC AAR93121;
XX DT 10-OCT-1996 (first entry)
XX DE Tilapia prolactin receptor (mature form).
XX KW Fish prolactin; tiPRL; receptor; hormone; agonist; antagonist;
XX KW reproductive cycle synchronisation; teleost; bony fish; Cypriniformes.
XX OS Oreochromis niloticus.
XX FH Key Location/Qualifiers
XX FT 1..606 /label= prolactin_receptor
XX FT Protein 1..210 /label= extracellular
XX FT Domain 68..70 /note= "comprises 5 Cys residues"
XX FT Modified-site 77..79 /label= glycosylation_site
XX FT Modified-site 77..79 /note= "potential"
XX FT Binding-site 192..196 /label= glycosylation_site
XX FT Binding-site 192..196 /note= "potential"
XX FT Domain 211..234 /label= ligand binding_motif
XX FT Domain 211..234 /note= "conforms to Trp-Ser-Xaa-Trp-Ser consensus"
XX FT Domain 235..606 /label= transmembrane
XX FT Domain 235..606 /label= cytoplasmic
XX FT Region 245..250 /note= "slightly longer than mammalian PRL receptor cytoplasmic domain"
XX FT Region 245..250 /label= Box_1
XX FN FR2724181-A1.
XX PD 08-MAR-1996.
XX PF 01-SEP-1994; 94FR-00010535.
XX PR 01-SEP-1994; 94FR-00010535.
XX PA (INRM ) INSRM INST NAT SANTE & RECH MEDICALE.
XX PI Kelly PA, Egerly M, Prunet P, Sandra O;
XX DR WPI; 1996-153124/16.
XX DR N-PSDB; AAT17141.
XX KW Fish prolactin receptor - useful for detecting prolactin agonists and antagonists.
XX PS Claim 5; Page 20-21; 35pp; French.
XX

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```

CC A cDNA sequence coding for a fish prolactin (PRL) receptor was isolated
CC from a Oreochromis niloticus (tilapia) kidney cDNA expression library
CC following screening with radioactive tiPRL. The cDNA insert was found to
CC contain an open reading frame for a 630 amino acid protein. The mature
CC protein (606 amino acids) has estimated mol. wt. 68.2 kDa and isoelectric
CC point 5.53. Transformed eukaryotic cells expressing the PRL receptor are
CC useful for identifying agonists and antagonists of PRL which have
CC potential applications in fish farming, e.g. for synchronising
CC reproductive cycles. The present sequence is that of the mature PRL
CC receptor from tilapia
XX
SQ Sequence 606 AA;
Query Match 47.1%; Score 549.5; DB.2; Length 606;
Best Local Similarity 54.6%; Pred. No. 2.2e-45;
Matches 101; Conservative 26; Mismatches 55; Indels 3; Gaps 3;
Qy 28 POKPEIFKCRSPNKETFTCWWRPGTGGGLPTNYSLTYHREGELTHCECPDYITGGNSCH 87
Db 5 POKPEIFKCRSPNKETFTCWWRPGTGGGLPTNYSLTYHREGELTHCECPDYITGGNSCH 64
Qy 88 POKQVTSWRYIIMVNATQ-MGSSFSDELYVDVTVYIVQDPDPLEAVEVKQPEDRKPYL 146
Db 65 FNKNNTLIWSYNTVWATNALGKTYSDQIDIVYIVQHPPEKLEVTVMK-DQGWPF 123
Qy 147 WIKSPPTLIDLKTGWFTLLYEIRIKPE-KAAEWEIHFAGQOTEFKILSLHPGQKYLQV 205
Db 124 RVSWEPKADTRSGWITLIYELRVKLEDESEWENHAAGQKMFSLSSGGTYLQV 183
Qy 206 RCKPD 210
Db 184 RCKPD 188

RESULT 15
AAR93120
ID AAR93120 standard; protein; 630 AA.
XX AC AAR93120;
XX DT 09-OCT-1996 (first entry)
XX DE Tilapia prolactin receptor precursor.
XX KW Fish prolactin; tiPRL; receptor; hormone; agonist; antagonist;
XX KW reproductive cycle synchronisation; teleost; bony fish; Cypriniformes.
XX OS Oreochromis niloticus.
XX FH Key Location/Qualifiers
XX FT 25..630 /label= prolactin_receptor
XX FT Protein 25..234 /label= extracellular
XX FT Domain 92..94 /note= "comprises 5 Cys residues"
XX FT Modified-site 92..94 /label= glycosylation_site
XX FT Modified-site 101..103 /note= "potential"
XX FT Modified-site 101..103 /label= glycosylation_site
XX FT Binding-site 216..220 /note= "potential"
XX FT Binding-site 216..220 /label= ligand binding_motif
XX FT /note= "conforms to trp-Ser-Xaa-Trp-Ser consensus"
XX FT Domain 235..258 /label= transmembrane
XX FT Domain 259..630 /label= cytoplasmic
XX FT /note= "slightly longer than mammalian PRL receptor cytoplasmic domain"
XX FT Region 269..274 /label= Box_1
XX FT /note= "proline-rich region highly conserved among

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receptors for cytokines, growth hormones and prolactin  
and is critical for signal transduction"

FR2724181-A1.

08-MAR-1996.

01-SEP-1994; 94FR-00010535.

01-SEP-1994; 94FR-00010535.

(INRM ) INSERM INST NAT SANTE &amp; RECH MEDICALE.

Kelly PA, Edery M, Prunet P, Sandra O;

WPI; 1996-153124/16.

N-PSDB; AAT17141.

Fish prolactin receptor - useful for detecting prolactin agonists and  
antagonists.

Example; Page 15-16; 35pp; French.

A cDNA sequence coding for a fish prolactin (PRL) receptor was isolated  
from a Oreochromis niloticus (tilapia) kidney cDNA expression library  
following screening with radioactive tPRL. The cDNA insert was found to  
contain an open reading frame for a 630 amino acid protein. The mature  
protein (606 amino acids) has estimated mol. wt. 68.2 kDa and isoelectric  
point 5.53. Transformed eukaryotic cells expressing the PRL receptor are  
useful for identifying agonists and antagonists of PRL which have  
potential applications in fish farming, e.g. for synchronising  
reproductive cycles. The present sequence is that of the precursor for  
the PRL receptor from tilapia

SQ Sequence 630 AA;

Query Match

Best Local Similarity 47.1%; Score 549.5; DB 2; Length 630;

Matches 101; Conservative 26; Mismatches 55; Indels 3; Gaps 3;

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Db 29 PGKPTIKCRSPKEFTCWRRGSDGGLPTTYALYYRKGSDVVECDVHTAGKNSCF 88

QY 88 FGQYTSMTWRTYIMVNATO-MGSEFSDLYVDVTYIVQDPPELAEVVKQPEDRKPYL 146

Db 89 FNKNNTLIWVSNITVYATNALGKTYSDPDIDVVIVQHPPEKLEVTVMK-DQGWPF 147

QY 147 WIKWSPTLIDKGTWFTLLYIRLKPE-KAAEWELHFAQQQTEPKILSLHPGQKYLIVQV 205

Db 148 RVSWEPKRAIRSGWITLIYELVKLEDESEWENHAGQQQMFNIFSLRSGGTLYIQV 207

QY 206 RCKPD 210

Db 208 RCKPD 212

Search completed: May 12, 2004, 16:17:27  
Job time : 62 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: May 12, 2004, 16:19:02 ; Search time 45 Seconds  
(without alignments)  
1295,312 Million cell updates/sec

Title: US-10-029-079-3  
Perfect score: 1166  
Sequence: 1 MKENVASATVFTLLFLNTCL.....KILSLHPGQKYLQVRCRKP 210

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	1166	100.0	210	13	US-10-029-079-3	Sequence 3, Appl 1
2	1155.5	99.1	622	12	US-10-058-270A-40	Sequence 40, Appl
3	1155.5	99.1	622	14	US-10-177-293-373	Sequence 373, Appl
4	1155.5	99.1	622	15	US-10-295-027-112	Sequence 112, Appl
5	1155.5	99.1	622	15	US-10-295-027-744	Sequence 744, Appl
6	987	84.6	597	12	US-10-287-971-74	Sequence 74, Appl
7	297	25.5	389	9	US-09-880-578-25	Sequence 25, Appl
8	297	25.5	389	9	US-09-880-578-26	Sequence 26, Appl
9	296	25.4	303	9	US-09-880-578-21	Sequence 21, Appl
10	296	25.4	385	9	US-09-880-578-20	Sequence 20, Appl
11	296	25.4	388	9	US-09-880-578-17	Sequence 17, Appl
12	296	25.4	389	9	US-09-880-578-27	Sequence 27, Appl
13	296	25.4	389	9	US-09-880-578-31	Sequence 31, Appl
14	296	25.4	422	9	US-09-880-578-2	Sequence 2, Appl 1
15	295	25.3	389	9	US-09-880-578-30	Sequence 30, Appl

16	294	25.2	389	9	US-09-880-578-24	Sequence 24, Appl
17	294	25.2	389	9	US-09-880-578-28	Sequence 28, Appl
18	294	25.2	389	9	US-09-880-578-29	Sequence 29, Appl
19	293	25.1	303	9	US-09-880-578-23	Sequence 23, Appl
20	293	25.1	350	9	US-09-037-657-25	Sequence 25, Appl
21	293	25.1	389	9	US-09-880-578-22	Sequence 22, Appl
22	293	25.1	392	9	US-09-880-578-18	Sequence 18, Appl
23	293	25.1	404	14	US-10-252-958-2	Sequence 2, Appl 1
24	293	25.1	410	14	US-10-247-463-4	Sequence 4, Appl 1
25	293	25.1	421	9	US-09-037-657-44	Sequence 44, Appl
26	293	25.1	422	9	US-09-866-028-32	Sequence 32, Appl
27	293	25.1	422	9	US-09-944-449-32	Sequence 32, Appl
28	293	25.1	422	9	US-09-944-457-32	Sequence 32, Appl
29	293	25.1	422	9	US-09-944-862-32	Sequence 32, Appl
30	293	25.1	422	9	US-09-945-587-32	Sequence 32, Appl
31	293	25.1	422	9	US-09-945-015-32	Sequence 32, Appl
32	293	25.1	422	9	US-09-944-396-32	Sequence 32, Appl
33	293	25.1	422	9	US-09-944-097-32	Sequence 32, Appl
34	293	25.1	422	9	US-09-944-432-32	Sequence 32, Appl
35	293	25.1	422	9	US-09-943-762-32	Sequence 32, Appl
36	293	25.1	422	9	US-09-944-654-32	Sequence 32, Appl
37	293	25.1	422	9	US-09-943-851A-32	Sequence 32, Appl
38	293	25.1	422	9	US-09-944-413-32	Sequence 32, Appl
39	293	25.1	422	9	US-09-944-403-32	Sequence 32, Appl
40	293	25.1	422	9	US-09-944-896-32	Sequence 32, Appl
41	293	25.1	422	9	US-09-944-944-32	Sequence 32, Appl
42	293	25.1	422	9	US-09-944-929-32	Sequence 32, Appl
43	293	25.1	422	9	US-09-944-907-32	Sequence 32, Appl
44	293	25.1	422	10	US-09-944-864-32	Sequence 32, Appl
45	293	25.1	422	10	US-09-944-852-32	Sequence 32, Appl

## ALIGNMENTS

RESULT 1  
US-10-029-079-3  
; Sequence 3, Application US/10029079  
; Publication No. US20020119154A1  
; GENERAL INFORMATION:  
; APPLICANT: Kline, J. Bradford  
; TITLE OF INVENTION: Composition and Method for Modulating Somatolactogenic Function  
; FILE REFERENCE: PENN-0795  
; CURRENT APPLICATION NUMBER: US/10/029,079  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/258,285  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 210  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-029-079-3

Query Match 100.0%; Score 1166; DB 13; Length 210;  
Best Local Similarity 100.0%; Pred. No. 1.9e-106;  
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKENVASATVFTLLFLNTCLNGOLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
Db 1 MKENVASATVFTLLFLNTCLNGOLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMMVNATQWGSFSDLYVDV 120  
Db 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMMVNATQWGSFSDLYVDV 120  
QY 121 TVIVOPDPLEAVKQPEKPYLWIKWSPTLIDIKTGWFTLLYIRLKPEKAAWE 180  
Db 121 TVIVOPDPLEAVKQPEKPYLWIKWSPTLIDIKTGWFTLLYIRLKPEKAAWE 180  
QY 181 IHFAGQQTFFKILSLHPGQKYLQVRCRKP 210

Db 181 IHFAGQOTEFKILSLHPGQKYLQVVRCKPD 210

RESULT 2

US-10-058-270A-40  
; Sequence 40, Application US/10058270A  
; Publication No. US20040029114A1  
; GENERAL INFORMATION:  
; APPLICANT: Mack, David H.  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and  
; TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer  
; FILE REFERENCE: 018501-005210US  
; CURRENT APPLICATION NUMBER: US/10/058,270A  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: US 60/263,965  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: US 60/265,928  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 09/829,472  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: US 60/282,698  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: US 60/288,590  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: US 60/294,443  
; PRIOR FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 622  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-058-270A-40

Query Match 99.1%; Score 1155.5; DB 12; Length 622;  
Best Local Similarity 99.5%; Pred. No. 7.7e-105;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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Db 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60  
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RESULT 3

US-10-177-293-373  
; Sequence 373, Application US/10177293  
; Publication No. US20030124128A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Gannavarpu, Manjula  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Mertens, Maureen  
; APPLICANT: Myer, Vic  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Xu, Yongyao

; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Monahan, John  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: Bast Jr., Robert C.  
; APPLICANT: Hortobagyi, Gabriel N.  
; APPLICANT: Puzstai, Lajos  
; APPLICANT: Meric, Funda  
; APPLICANT: Sahin, Aysegul  
; APPLICANT: Mills, Gordon B.  
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,  
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER  
; FILE REFERENCE: MRI-038  
; CURRENT APPLICATION NUMBER: US/10/177,293  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 60/299,887  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: US 60/301,572  
; PRIOR FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: US 60/306,501  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: US 60/325,002  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 60/362,585  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 373  
; LENGTH: 622  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-177-293-373

Query Match 99.1%; Score 1155.5; DB 14; Length 622;  
Best Local Similarity 99.5%; Pred. No. 7.7e-105;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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Db 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60  
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Qy 120 VTIYVQDPPLELAWEKQEDSKPYLWIKWSPTLLDLKTGWFTLLYIRLKPKEAAEW 179  
Db 121 VTIYVQDPPLELAWEKQEDSKPYLWIKWSPTLLDLKTGWFTLLYIRLKPKEAAEW 180  
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Db 181 EHPAGQOTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 4

US-10-295-027-112  
; Sequence 112, Application US/10295027  
; Publication No. US20030232350A1  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsberg, Wendy M.  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Glynn, Richard  
; APPLICANT: Hevezi, Peter A.  
; APPLICANT: Mack, David H.  
; APPLICANT: Murray, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
; FILE REFERENCE: 018501-012500US

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; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 622
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-10-295-027-112

Query Match          99.1%; Score 1155.5; DB 15; Length 622;
Best Local Similarity 99.5%; Pred. No. 7.7e-105;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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D5 61 SLVYHREGETLMHECPDYITGGNSCHFGKQYTSWRTYIMVNATQMGSSFSDELVD 120
QY 120 VTYIVQDPPLLEAVEVQKPEDRKPYLWIKWSPPTLIDLKTGWFTLLYELRLKPEKAAEW 179
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RESULT 5
US-10-295-027-744
; Sequence 744, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; METHODS OF SCREENING: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
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; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
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; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 744
; LENGTH: 622
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-10-295-027-744

Query Match          99.1%; Score 1155.5; DB 15; Length 622;
Best Local Similarity 99.5%; Pred. No. 7.7e-105;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVTLILLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
D5 1 MKENVASATVTLILLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
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D5 61 SLVYHREGETLMHECPDYITGGNSCHFGKQYTSWRTYIMVNATQMGSSFSDELVD 120
QY 120 VTYIVQDPPLLEAVEVQKPEDRKPYLWIKWSPPTLIDLKTGWFTLLYELRLKPEKAAEW 179
D5 121 VTYIVQDPPLLEAVEVQKPEDRKPYLWIKWSPPTLIDLKTGWFTLLYELRLKPEKAAEW 180
QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCRKP 210
D5 181 EHFAGQOTEFKILSLHPGQKYLQVRCRKP 211

RESULT 6
US-10-287-971-74
; Sequence 74, Application US/10287971
; Publication No. US20040067882A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-480A
; CURRENT APPLICATION NUMBER: US/10/287,971
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
```

; PRIOR APPLICATION NUMBER: 60/406,181  
; PRIOR FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 397  
; SOFTWARE: Curaseq1ist version 0.1  
; SEQ ID NO 74  
; LENGTH: 597  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-287-971-74

Query Match 84.68; Score 987; DB 12; Length 597;  
Best Local Similarity 87.78; Pred. No. 2.7e-88;  
Matches 185; Conservative 0; Mismatches 26; Gaps 2;  
QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGPKPEIFKCRSPNKETFTTCWRPFGTDGGLPTNY 60  
DB 1 MKNVASATVFTLLFLNTCLLNGQLPPGPKPEIFKCRSPNKETFTTCWRPFGTDGGLPT-- 58  
QY 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMTWRTYIMMNVNAT-QMGSSFSDELYVD 119  
DB 59 -----NSCHFGKQYTSMTWRTYIMMNVNATNQMGSSFSDELYVD 95  
QY 120 VTIVVQDPPLLEAVEVKQPEDRKPYLWIKWSPTTLDLKTGWFTLLYRILKPEKAAEW 179  
DB 96 VTIVVQDPPLLEAVEVKQPEDRKPYLWIKWSPTTLDLKTGWFTLLYRILKPEKAAEW 155  
QY 180 EHFAGQOTBFKLSLHPGQKYLQVRCRKP 210  
DB 156 EHFAGQOTBFKLSLHPGQKYLQVRCRKP 186

## RESULT 7

US-09-880-578-25  
; Sequence 25, Application US/09880578  
; Patent No. US20020045733A1  
; GENERAL INFORMATION:

APPLICANT: Lok, Si

Presnell, Scott R.  
Jelmsberg, Anna C.  
Gilbert, Teresa  
Foster, Donald C.  
Adams, Robyn L.  
Lehner, Joyce M.

TITLE OF INVENTION: MAMMALIAN ZCYTORS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics  
STREET: 1201 Eastlake Ave East  
CITY: Seattle  
STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/880,578

FILING DATE: 13-Jun-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: &lt;Unknown&gt;

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX: &lt;Unknown&gt;

INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 389 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-09-880-578-25

Query Match 25.58; Score 297; DB 9; Length 389;  
Best Local Similarity 38.08; Pred. No. 1.1e-20;  
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;  
QY 15 LFLNTCLLNGQLPPGPKPEIFKCRSPNKETFTTCWRPFGTDGG--LPTNYSILTYHREGETLM 72  
DB 86 ILAGSCLYVG-LPEKPVNISCHSKNMKDLTCRWTPGAHGETFLHTNYSLYKYLKRWGQD 144  
QY 73 HECPDYITGGNSCHFGKQYTSMTWRTYIMMNVNAT-QMGSSFSDELYVDVTVIVQDPPLLE 131  
DB 145 NTCEDYHTVGFHSCHIKPD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTDDPPD 203  
QY 132 LAV-EVKQPEDRKPYLWIKWSPTTLDLKTGWFTLLYRILKPEKAAEW-IHFAGQOTE 189  
DB 204 VHSRVGLEDQLSVRVV--SPFALKDF---LFQAKYQIRYRVEDSDVWKVVDVDSNQT 258  
QY 190 FKLSLHPGQKYLQVRCRKP 209  
DB 259 CRLAGLKPSTVYFVQVRCNP 278

## RESULT 8

US-09-880-578-26

; Sequence 26, Application US/09880578  
; Patent No. US20020045733A1  
; GENERAL INFORMATION:

APPLICANT: Lok, Si

Presnell, Scott R.  
Jelmsberg, Anna C.  
Gilbert, Teresa  
Foster, Donald C.  
Adams, Robyn L.  
Lehner, Joyce M.

TITLE OF INVENTION: MAMMALIAN ZCYTORS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics  
STREET: 1201 Eastlake Ave East  
CITY: Seattle  
STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/880,578

FILING DATE: 13-Jun-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: &lt;Unknown&gt;

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX: &lt;Unknown&gt;

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-880-578-26

Query Match      25.5%; Score 297; DB 9; Length 389;
Best Local Similarity 38.0%; Pred. No. 1.1e-20;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFLNTCLLNGQLPCKEPIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTTHREGETLM 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 86 ILAGSCLVYG-LPPEKPVNISCSKMKDLTCRWTPCAHGETFLHTNYSLKYLKRWYQD 144
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 HECPDYITGGPNSCHFGKQYTSMWRTYIMVNAT-QMGSFSDLYVDVTVIVQDPPLP 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 145 NTCEEVHTVGHPSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDILDVTTDPPD 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 LAV-EVKQPEDRKPYLWIKMSPTLIDLKTGWFLLYEIRLKPEKAAEWE-IHFAGQOTE 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 204 VHSVSRVGGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVSDVDWKVDDVSNQTS 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 FKILSLHPGQKYLVOVRCKP 209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 259 CRLAGLKPGTVYFVQVRCNP 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-09-880-578-21
; Sequence 21, Application US/09880578
; Patent No. US20020045733A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; Presnell, Scott R.
; Jelmeberg, Anna C.
; Gilbert, Teresa
; Foster, Donald C.
; Adams, Robyn L.
; Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-880-578-21

Query Match      25.4%; Score 296; DB 9; Length 303;
Best Local Similarity 38.0%; Pred. No. 1.1e-20;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFLNTCLLNGQLPCKEPIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTTHREGETLM 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 86 ILAGSCLVYG-LPPEKPVNISCSKMKDLTCRWTPCAHGETFLHTNYSLKYLKRWYQD 144
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 HECPDYITGGPNSCHFGKQYTSMWRTYIMVNAT-QMGSFSDLYVDVTVIVQDPPLP 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 145 NTCEEVHTVGHPSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDILDVTTDPPD 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 LAV-EVKQPEDRKPYLWIKMSPTLIDLKTGWFLLYEIRLKPEKAAEWE-IHFAGQOTE 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 204 VHSVSRVGGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVSDVDWKVDDVSNQTS 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 FKILSLHPGQKYLVOVRCKP 209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 259 CRLAGLKPGTVYFVQVRCNP 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-09-880-578-20
; Sequence 20, Application US/09880578
; Patent No. US20020045733A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; Presnell, Scott R.
; Jelmeberg, Anna C.
; Gilbert, Teresa
; Foster, Donald C.
; Adams, Robyn L.
; Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-880-578-20

Query Match      25.4%; Score 296; DB 9; Length 385;
Best Local Similarity 38.0%; Pred. No. 1.4e-20;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETPTCWRPQTDGG--LPNYSILTYHREGETLM 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 86 ILAGSCLVVG-LPPEKPVNISCSKNMKDLTCRTWTPGAHGETLHTNYSILKYKLRWYGQD 144
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 HECPDYITGPNCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTVYIVQDDPPPLE 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 145 NTCBEYHTVGPCHSPKDK-LALFTPYEINWEATNLGARSADVLTLDILDVVTTPDPPPE 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 LAV-EVKQPEDRKPYLWIKWSPPTLIDLTGWFTLLYEIRLKPEKAAEWE-IHFAGQOQTE 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 204 VHVSRVGGLEDQLSVRWV--SPALKDF---LFQAKYQIYRYVEDSDVKWVDDVSNQTS 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 FKILSLHPGQKYLIVQVRCKP 209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 259 CRLAGLKPGTVYFVQVRCNP 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-09-880-578-17
; Sequence 17, Application US/09880578
; Patent No. US20020045733A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; Presnell, Scott R.
; Jelmeberg, Anna C.
; Gilbert, Teresa
; Foster, Donald C.
; Adams, Robyn L.
; Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-880-578-17

Query Match      25.4%; Score 296; DB 9; Length 388;
Best Local Similarity 38.0%; Pred. No. 1.4e-20;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETPTCWRPQTDGG--LPTNYSILTYHREGETLM 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 89 ILAGSCLVVG-LPPEKPVNISCSKNMKDLTCRTWTPGAHGETLHTNYSILKYKLRWYGQD 147
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 HECPDYITGPNCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTVYIVQDDPPPLE 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 148 NTCBEYHTVGPCHSPKDK-LALFTPYEINWEATNLGARSADVLTLDILDVVTTPDPPPE 206
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 LAV-EVKQPEDRKPYLWIKWSPPTLIDLTGWFTLLYEIRLKPEKAAEWE-IHFAGQOQTE 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 207 VHVSRVGGLEDQLSVRWV--SPALKDF---LFQAKYQIYRYVEDSDVKWVDDVSNQTS 261
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 FKILSLHPGQKYLIVQVRCKP 209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 262 CRLAGLKPGTVYFVQVRCNP 281
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
US-09-880-578-27
; Sequence 27, Application US/09880578
; Patent No. US20020045733A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; Presnell, Scott R.
; Jelmeberg, Anna C.
; Gilbert, Teresa
; Foster, Donald C.
; Adams, Robyn L.
; Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```



```
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-880-578-27

Query Match      25.4%; Score 296; DB 9; Length 389;
Best Local Similarity 38.0%; Pred. No. 1.4e-20;
Matches       76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY   15 LFLNLTCLLNGQLPPGKPEIFKCSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM 72
     :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB   86 ILAGSGLVYG-LPPEKPVNISCSKNMKDLTCRWTPGAHGTEFLTHTNSLYKLRYWGD 144
     :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY   73 HECPDYITGPNSCHFGKYQTSMWTYIMMNAT-QMGSSFSDELYVDVTIVDPDPLE 131
     :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB   145 NTCEEYHTVGPHSCHIPKD-LALFPTYEIWEATNLGSRSDDLTLILDVTTDDPPD 203
     :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY   132 LAV-EVKPEDRKPYLIWKMSPTTLDLTGTWFTLLYEIRLKPEKAAEWE-IHFAGQOTE 189
     :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB   204 VHVSRVGGLEDQLSVRNV--SPALKDF---LFQAQYQIRVRVEDSDVMKVVDVSNQTS 258
     :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY   190 FKILSLHPGQKYLVOVRCKP 209
     :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB   259 CRLIGLKGTVYFVQRCPNP 278
     :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-880-578-31
; Sequence 31, Application US/09880578
; Patent No. US20020045733A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; Presnell, Scott R.
; Jelmeberg, Anna C.
; Gilbert, Teresa
; Foster, Donald C.
; Adams, Robyn L.
; Lehner, Joyce M.
; TITLE OF INVENTION: NANNALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zylogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunz, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
```



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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:17:31 ; Search time 183 Seconds  
(without alignments)  
1120.061 Million cell updates/sec

Title: US-10-029-079-3

Perfect score: 1166

Sequence: 1 MKENVASATVFILLLELNTC.....KILSLHPGKYLIVQVRCPD 210

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Parents AA Main:

- 1: /cgn2\_6/prodata/2/paa/US06 COMB.pcp.\*
- 2: /cgn2\_6/prodata/2/paa/US06 COMB.pcp.\*
- 3: /cgn2\_6/prodata/2/paa/US07 COMB.pcp.\*
- 4: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 5: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 6: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 7: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 8: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 9: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 10: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 11: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 12: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
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- 14: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 15: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
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- 19: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
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- 26: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 27: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 28: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 29: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 30: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 31: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 32: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*
- 33: /cgn2\_6/prodata/2/paa/US08 COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
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1	1166	100.0	210	26	US-10-029-079-3	Sequence 3, Appli
2	1155.5	99.1	230	21	US-09-724-676-83309	Sequence 83309, A
3	1155.5	99.1	230	21	US-09-724-676A-83309	Sequence 83309, A
4	1155.5	99.1	288	33	US-60-452-680-22670	Sequence 22670, A
5	1155.5	99.1	349	22	US-09-791-537-37838	Sequence 37838, A
6	1155.5	99.1	349	22	US-09-791-537-37838	Sequence 22672, A
7	1155.5	99.1	376	33	US-60-452-680-22671	Sequence 22671, A
8	1155.5	99.1	426	21	US-09-724-676-83308	Sequence 83308, A
9	1155.5	99.1	426	21	US-09-724-676A-83308	Sequence 83308, A
10	1155.5	99.1	622	1	PCT-US01-49049-3	Sequence 3, Appli
11	1155.5	99.1	622	1	PCT-US01-49049A-3	Sequence 3, Appli
12	1155.5	99.1	622	1	PCT-US02-19669-373	Sequence 373, App
13	1155.5	99.1	622	1	PCT-US02-19669A-373	Sequence 373, App
14	1155.5	99.1	622	22	US-09-791-537-18829	Sequence 18829, A
15	1155.5	99.1	622	26	US-10-058-270A-40	Sequence 40, Appl
16	1155.5	99.1	622	27	US-10-177-293-373	Sequence 373, App
17	1155.5	99.1	622	28	US-10-395-027-112	Sequence 112, App
18	1155.5	99.1	622	28	US-10-395-027-744	Sequence 744, App
19	1155.5	99.1	622	33	US-60-452-680-22669	Sequence 22669, A
20	1155.5	99.1	637	24	US-09-949-016-10128	Sequence 10128, A
21	1052.5	90.3	622	22	US-09-791-537-3751	Sequence 3751, Ap
22	1036.5	88.9	206	22	US-09-791-537-24513	Sequence 24513, A
23	1036.5	88.9	211	7	US-08-310-552-2	Sequence 2, Appli
24	1036.5	88.9	211	22	US-09-791-537-116008	Sequence 116008, A
25	987	84.6	597	28	US-10-287-971-74	Sequence 74, Appl
26	935.5	80.2	616	22	US-09-791-537-99548	Sequence 99548, A
27	901.5	77.3	581	22	US-09-791-537-119333	Sequence 119333, A
28	888.5	76.2	625	22	US-09-791-537-23820	Sequence 23820, A
29	865.5	74.2	296	22	US-09-791-537-53150	Sequence 53150, A
30	865.5	74.2	581	22	US-09-791-537-119332	Sequence 119332, A
31	863.5	74.1	296	22	US-09-791-537-107221	Sequence 107221, A
32	863.5	74.1	581	22	US-09-791-537-36028	Sequence 36028, A
33	837	71.8	310	22	US-09-791-537-85473	Sequence 85473, A
34	837	71.8	412	22	US-09-791-537-93032	Sequence 93032, A
35	813.5	69.8	292	22	US-09-791-537-62081	Sequence 62081, A
36	813.5	69.8	303	22	US-09-791-537-62063	Sequence 62063, A
37	813.5	69.8	608	22	US-09-791-537-35679	Sequence 35679, A
38	813.5	69.8	608	22	US-09-791-537-64104	Sequence 64104, A
39	799.5	68.6	210	22	US-09-791-537-86333	Sequence 86333, A
40	764.5	65.6	198	22	US-09-791-537-95162	Sequence 95162, A
41	688.5	59.0	831	22	US-09-791-537-49689	Sequence 49689, A
42	683.5	58.6	217	22	US-09-791-537-96201	Sequence 96201, A
43	683.5	58.6	830	22	US-09-791-537-119338	Sequence 119338, A
44	682	58.5	831	22	US-09-791-537-119339	Sequence 119339, A
45	679	58.2	134	12	US-08-806-597-8	Sequence 8, Appli

## ALIGNMENTS

RESULT 1  
US-10-029-079-3  
; Sequence 3, Application US/10029079  
; GENERAL INFORMATION:  
; APPLICANT: Clevenger, Charles V  
; TITLE OF INVENTION: Composition and Method for Modulating Somatolactogenic Function  
; FILE REFERENCE: PENN-0795  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/258,285  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 3  
; LENGTH: 210  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-029-079-3

Query Match 100.0%; Score 1166; DB 26; Length 210;  
Best Local Similarity 100.0%; Pred.No. 3.6e-118;  
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60  
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Db 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60  
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Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWTYIMMNVNAT-QMGSSFSDELVD 120  
QY 121 TYIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYEIRLKPEKAAEW 180  
Db 121 TYIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYEIRLKPEKAAEW 180  
QY 181 IHFAGQOTEFKILSLHPGQKYLQVRCRCPD 210  
Db 181 IHFAGQOTEFKILSLHPGQKYLQVRCRCPD 210

## RESULT 2

US-09-724-676-83309  
; Sequence 83309, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 83309  
; LENGTH: 230  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676-83309

Query Match 99.1%; Score 1155.5; DB 21; Length 230;  
Best Local Similarity 99.5%; Pred. No. 5.7e-117;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWTYIMMNVNAT-QMGSSFSDELVD 120  
QY 120 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYEIRLKPEKAAEW 179  
Db 121 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYEIRLKPEKAAEW 180  
QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 210  
Db 181 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 211

## RESULT 3

US-09-724-676A-83309  
; Sequence 83309, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 83309  
; LENGTH: 230  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676A-83309

Query Match 99.1%; Score 1155.5; DB 21; Length 230;  
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Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWTYIMMNVNAT-QMGSSFSDELVD 119  
Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWTYIMMNVNAT-QMGSSFSDELVD 120  
QY 120 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYEIRLKPEKAAEW 179  
Db 121 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYEIRLKPEKAAEW 180  
QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 210  
Db 181 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 211

## RESULT 3

US-09-724-676A-83309  
; Sequence 83309, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 83309  
; LENGTH: 230  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676A-83309

Query Match 99.1%; Score 1155.5; DB 21; Length 230;  
Best Local Similarity 99.5%; Pred. No. 5.7e-117;  
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Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWTYIMMNVNAT-QMGSSFSDELVD 120  
QY 120 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYEIRLKPEKAAEW 179  
Db 121 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYEIRLKPEKAAEW 180  
QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 210  
Db 181 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 211

## RESULT 4

US-60-452-680-22670  
; Sequence 22670, Application US/60452680  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: GRUPE, Andrew  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01450  
; CURRENT APPLICATION NUMBER: US/60/452,680  
; CURRENT FILING DATE: 2003-03-07  
; NUMBER OF SEQ ID NOS: 116213  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22670  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-452-680-22670

Query Match 99.1%; Score 1155.5; DB 33; Length 288;  
Best Local Similarity 99.5%; Pred. No. 7.7e-117;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWTYIMMNVNAT-QMGSSFSDELVD 119  
Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWTYIMMNVNAT-QMGSSFSDELVD 120  
QY 120 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYEIRLKPEKAAEW 179  
Db 121 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYEIRLKPEKAAEW 180  
QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 210  
Db 181 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 211

## RESULT 5

US-09-791-537-37838  
; Sequence 37838, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22

US-09-791-537-37838  
; Sequence 37838, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22

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; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37838
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-37838

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Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 179
DB 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 180
QY 180 EHFAGQOQTEFKILSLHPGQKYLQVVRCKPD 210
DB 181 EHFAGQOQTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 6
US-60-452-680-22672
; Sequence 22672, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 22672
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-22672

Query Match
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Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 179
DB 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 180
QY 180 EHFAGQOQTEFKILSLHPGQKYLQVVRCKPD 210
DB 181 EHFAGQOQTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 7
US-60-452-680-22671
; Sequence 22671, Application US/60452680
; GENERAL INFORMATION:

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; APPLICANT: CARGILL, Michele
; APPLICANT: GROPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22671
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-22671

Query Match
Best Local Similarity 99.1%; Score 1155.5; DB 33; Length 376;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 179
DB 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 180
QY 180 EHFAGQOQTEFKILSLHPGQKYLQVVRCKPD 210
DB 181 EHFAGQOQTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 8
US-09-724-676-83308
; Sequence 83308, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83308
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-83308

Query Match
Best Local Similarity 99.1%; Score 1155.5; DB 21; Length 426;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 179
DB 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 180
QY 180 EHFAGQOQTEFKILSLHPGQKYLQVVRCKPD 210
DB 181 EHFAGQOQTEFKILSLHPGQKYLQVVRCKPD 211

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RESULT 9  
US-09-724-676A-83308  
; Sequence 83308, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Comugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 83308  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US01-49049-3

Query Match 99.1%; Score 1155.5; DB 21; Length 426;  
Best Local Similarity 99.5%; Pred. No. 1.3e-116;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Qy 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
Db 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
Qy 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMMVNAT-QMGSSFSDELYVD 119  
Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMMVNAT-QMGSSFSDELYVD 120  
Qy 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWKWSPPTLIDLTGWTLLYIRLKPKEAAEW 179  
Db 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWKWSPPTLIDLTGWTLLYIRLKPKEAAEW 180  
Qy 180 EHFAGQQTTEFKILSLHPGQKYLQVVRCKPD 210  
Db 181 EHFAGQQTTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 10  
PCT-US01-49049-3  
; Sequence 3, Application PC/TUS0149049  
; GENERAL INFORMATION:  
; APPLICANT: Genaisance Pharmaceuticals, Inc.  
; APPLICANT: Bieglecki, Karyn M  
; APPLICANT: Duda, Amy  
; APPLICANT: Koshv, Beena  
; TITLE OF INVENTION: HAPLOTYPES OF THE PRLR GENE  
; FILE REFERENCE: PRLR\_MWH-0892PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/49049  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/256,523  
; PRIOR FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 622  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US01-49049-3

Query Match 99.1%; Score 1155.5; DB 1; Length 622;  
Best Local Similarity 99.5%; Pred. No. 2.2e-116;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Qy 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
Db 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
Qy 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMMVNAT-QMGSSFSDELYVD 119  
Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMMVNAT-QMGSSFSDELYVD 120

Qy 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWKWSPPTLIDLTGWTLLYIRLKPKEAAEW 179  
Db 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWKWSPPTLIDLTGWTLLYIRLKPKEAAEW 180  
Qy 180 EHFAGQQTTEFKILSLHPGQKYLQVVRCKPD 210  
Db 181 EHFAGQQTTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 11  
PCT-US01-49049A-3  
; Sequence 3, Application PC/TUS0149049A  
; GENERAL INFORMATION:  
; APPLICANT: Genaisance Pharmaceuticals, Inc.  
; APPLICANT: Bieglecki, Karyn M  
; APPLICANT: Duda, Amy  
; APPLICANT: Koshv, Beena  
; TITLE OF INVENTION: HAPLOTYPES OF THE PRLR GENE  
; FILE REFERENCE: PRLR\_MWH-0892PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/49049A  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/256,523  
; PRIOR FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 622  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US01-49049A-3

Query Match 99.1%; Score 1155.5; DB 1; Length 622;  
Best Local Similarity 99.5%; Pred. No. 2.2e-116;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Qy 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
Db 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
Qy 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMMVNAT-QMGSSFSDELYVD 119  
Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMMVNAT-QMGSSFSDELYVD 120  
Qy 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWKWSPPTLIDLTGWTLLYIRLKPKEAAEW 179  
Db 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWKWSPPTLIDLTGWTLLYIRLKPKEAAEW 180  
Qy 180 EHFAGQQTTEFKILSLHPGQKYLQVVRCKPD 210  
Db 181 EHFAGQQTTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 12  
PCT-US02-19669-373  
; Sequence 373, Application PC/TUS0219669  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.  
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,  
; FILE REFERENCE: MRI-038FC  
; CURRENT APPLICATION NUMBER: PCT/US02/19669  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 60/299,887  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: US 60/301,572  
; PRIOR FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: US 60/306,501  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: US 60/325,002  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 60/362,585  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx

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; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-19669-373

Query Match          99.1%; Score 1155.5; DB 1; Length 622;
Best Local Similarity 99.5%; Pred. No. 2.2e-116;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMMNVAT-QMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMMNVATQMGSSFSDELYVD 120
QY 120 VTYIVQDDPPLLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 179
DB 121 VTYIVQDDPPLLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 180
QY 180 EIHFAQQOTEFKILSLHHPGQKYLQVVRCKPD 210
DB 181 EIHFAQQOTEFKILSLHHPGQKYLQVVRCKPD 211

RESULT 13
PCT-US02-19669A-373
; Sequence 373, Application PC/TUS0219669A
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038PC
; CURRENT APPLICATION NUMBER: PCT/US02/19669A
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-19669A-373

Query Match          99.1%; Score 1155.5; DB 1; Length 622;
Best Local Similarity 99.5%; Pred. No. 2.2e-116;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMMNVAT-QMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMMNVATQMGSSFSDELYVD 120
QY 120 VTYIVQDDPPLLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 179
DB 121 VTYIVQDDPPLLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 180
QY 180 EIHFAQQOTEFKILSLHHPGQKYLQVVRCKPD 210
DB 181 EIHFAQQOTEFKILSLHHPGQKYLQVVRCKPD 211
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DB 121 VTYIVQDDPPLLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 180
QY 180 EIHFAQQOTEFKILSLHHPGQKYLQVVRCKPD 210
DB 181 EIHFAQQOTEFKILSLHHPGQKYLQVVRCKPD 211

RESULT 14
US-09-791-537-18829
; Sequence 18829, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18829
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-18829

Query Match          99.1%; Score 1155.5; DB 22; Length 622;
Best Local Similarity 99.5%; Pred. No. 2.2e-116;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMMNVAT-QMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMMNVATQMGSSFSDELYVD 120
QY 120 VTYIVQDDPPLLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 179
DB 121 VTYIVQDDPPLLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 180
QY 180 EIHFAQQOTEFKILSLHHPGQKYLQVVRCKPD 210
DB 181 EIHFAQQOTEFKILSLHHPGQKYLQVVRCKPD 211

RESULT 15
US-10-058-270A-40
; Sequence 40, Application US/10058270A
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Afar, Daniel
; APPLICANT: Bos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer
; FILE REFERENCE: 018501-0052100S
; CURRENT APPLICATION NUMBER: US/10/058,270A
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,965
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/265,928
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/829,472
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/282,698
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/288,590
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,443
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; PRIOR FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 622  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-058-270A-40

Query Match 99.1%; Score 1155.5; DB 26; Length 622;  
Best Local Similarity 99.5%; Pred. No. 2.2e-116;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Qy 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
Db 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
Qy 61 SLTYHREGELMHCEPDYITGGPNSCHFGKQYTSMMRTYIMVNAT-OMGSSFSDELYVD 119  
Db 61 SLTYHREGELMHCEPDYITGGPNSCHFGKQYTSMMRTYIMVNAT-OMGSSFSDELYVD 120  
Qy 120 VTIVVQDPPELEAVEVKQPEDRKPYLWIKWSPTTLDLKTGWFTLLYIIRLKPEKAAEW 179  
Db 121 VTIVVQDPPELEAVEVKQPEDRKPYLWIKWSPTTLDLKTGWFTLLYIIRLKPEKAAEW 180  
Qy 180 EIHFAQOOTEFKILSLHPGQKYLQVRCRKP 210  
Db 181 EIHFAQOOTEFKILSLHPGQKYLQVRCRKP 211

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Job time : 184 secs



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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:18:01 ; Search time 20 Seconds  
(without alignments)  
365.723 Million cell updates/sec

Title: US-10-029-079-3  
Perfect score: 1166  
Sequence: 1 MKENVASATVFILLFLNTC.....KILSLHPGQKYLQVRCKPD 210

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 235879 seqs, 34830801 residues

Total number of hits satisfying chosen parameters: 235879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	293	25.1	410	US-10-778-002-12	Sequence 12, Appl
2	293	25.1	422	US-10-821-801-794	Sequence 794, Appl
3	292	25.0	405	US-09-736-842-2	Sequence 2, Appl
4	292	25.0	407	US-10-778-002-13	Sequence 13, Appl
5	292	25.0	425	US-10-603-151-2	Sequence 2, Appl
6	273	23.4	434	US-09-736-842-4	Sequence 4, Appl
7	273	23.4	448	US-09-736-842-6	Sequence 6, Appl
8	262.5	22.5	202	US-10-806-655-4	Sequence 4, Appl
9	262.5	22.5	203	US-10-806-655-3	Sequence 3, Appl
10	262.5	22.5	206	US-10-806-655-2	Sequence 2, Appl
11	262.5	22.5	237	US-10-806-655-1	Sequence 1, Appl
12	262.5	22.5	638	PCT-US04-02188-142	Sequence 142, App
13	262.5	22.5	638	US-10-764-425-142	Sequence 142, App
14	262.5	22.5	638	US-10-821-801-503	Sequence 503, App
15	190.5	16.3	837	US-10-659-295-35	Sequence 35, Appl
16	165	14.2	918	US-10-667-290-3	Sequence 3, Appl
17	165	14.2	918	US-10-667-289-3	Sequence 3, Appl
18	163	14.0	836	US-10-659-295-34	Sequence 34, Appl
19	163	14.0	836	US-10-821-234-1559	Sequence 1559, Ap
20	161	13.8	379	US-10-779-890-11	Sequence 11, Appl
21	153	13.1	422	PCT-US04-02188-137	Sequence 137, App
22	153	13.1	422	US-10-764-425-137	Sequence 137, App
23	126	10.8	378	US/09/077	Sequence 12, Appl
24	126	10.8	380	US-09-077-817D-2	Sequence 2, Appl
25	125	10.7	662	US-10-772-531-54	Sequence 54, Appl
26	125	10.7	764	US-10-772-531-69	Sequence 69, Appl

27 122 10.5 239 6 US-10-772-531-22 Sequence 22, Appl  
28 122 10.5 324 6 US-10-772-531-18 Sequence 18, Appl  
29 122 10.5 649 6 US-10-772-531-46 Sequence 46, Appl  
30 122 10.5 732 6 US-10-772-531-2 Sequence 2, Appl  
31 114 9.8 1204 6 US-10-712-124-100 Sequence 100, App  
32 113.5 9.7 427 5 US-09-077-817D-4 Sequence 4, Appl  
33 111.5 9.6 1518 1 PCT-US04-07412-580 Sequence 580, App  
34 110 9.4 229 6 US-10-777-790-10 Sequence 10, Appl  
35 108.5 9.3 547 6 US-10-772-531-93 Sequence 93, Appl  
36 108.5 9.3 662 6 US-10-772-531-57 Sequence 57, Appl  
37 108.5 9.3 906 7 US-60-548-091-413 Sequence 413, App  
38 108.5 9.3 958 7 US-60-548-091-414 Sequence 414, App  
39 108.5 9.3 1165 7 US-60-548-091-412 Sequence 412, App  
40 108.5 9.3 1165 7 US-60-548-091-415 Sequence 415, App  
41 103.5 8.9 862 6 US-10-687-290-4 Sequence 4, Appl  
42 103.5 8.9 862 6 US-10-687-289-4 Sequence 4, Appl  
43 103.5 8.9 862 6 US-10-797-157-7 Sequence 7, Appl  
44 103.5 8.9 862 6 US-10-370-715B-68 Sequence 68, Appl  
45 102.5 8.8 507 1 PCT-US04-09416-2 Sequence 2, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-778-002-12  
; Sequence 12, Application US/10778002  
; GENERAL INFORMATION:  
; APPLICANT: Oppmann, Birgit  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; FILE REFERENCE: DX0935K  
; CURRENT APPLICATION NUMBER: US/10/778,002  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/521,335  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: primate  
US-10-778-002-12

Query Match 25.1%; Score 293; DB 6; Length 410;  
Best Local Similarity 37.5%; Pred. No. 3.5e-20;  
Matches 75; Conservative 28; Mismatches 85; Indels 12; Gaps 8;  
QY 15 LFLNTCLLNGQLPGKPEIFKCRSPENKETTFTCWPRGTDGG--LPTNYSLYTHREGETLM 72  
Db 123 ILAGSCLYVG-LPPEKPVNI SCWSKNMKDLTCRWTPGAHGETFLHTNYSLYKLRWYQDD 181  
QY 73 HECPDYITGGNSCHFGKQYTSMTWTYIMYNAT--OMGSSFSDELYVDVTIVQDPDPLE 131  
Db 182 NTCEYHVTGPHSCHIPKD--IALFTPYEIVWEATNRLGARSADVLTLLDLDVTTDPPD 240  
QY 132 LAV-EVKQPEPRKPKYLWIKWSPPPTLIDLKGTWFTLYEIRLKPEKAAEWE-IHFAGQOTE 189  
Db 241 VHVSRVGGLEDQLSVRWV--SPPALKDF--LFAQKYQIRYRVEDSDVKVVDVSNQTS 295  
QY 190 FKLSLHPGQKYLQVRCKP 209  
Db 296 CRLAGLKPGTVYFVQVRCNP 315

##### RESULT 2

US-10-821-801-794  
; Sequence 794, Application US/10821801  
; GENERAL INFORMATION:  
; APPLICANT: Hinzmann, Bernd  
; APPLICANT: Rosenthal, Andre

```

; APPLICANT: Hermann, Klaus
; APPLICANT: Heiden, Esmeralda
; APPLICANT: Pilarzsky, Christian
; APPLICANT: Brummendorf, Thomas
; APPLICANT: Staub, Eike
; APPLICANT: Ropcke, Stefan
; APPLICANT: Mennerich, Detlev
; APPLICANT: Kinnemann, Henrik
; APPLICANT: Li, Xinzhang
; TITLE OF INVENTION: Human nucleic acid sequences from lung tumours
; FILE REFERENCE: 00154/002001
; CURRENT APPLICATION NUMBER: US/10/821,801
; CURRENT FILING DATE: 2004-04-09
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 794
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-821-801-794

Query Match      25.1%; Score 293; DB 6; Length 422;
Best Local Similarity 37.5%; Pred. No. 3.6e-20;
Matches 75; Conservative 28; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFNLTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDG--LPTNYSLTYYHREGETLM 72
Db 123 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGD 181
QY 73 HECPDYITGGPNSCHFGKQYTSWRTYIMMVNAT-QMGSSFSDELYVDVTVIYQDPDPLE 131
Db 182 NTCEEYHTVGPHSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPPD 240
QY 132 LAV-EVKQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKEPEKAAWE-IHFAGQOTE 189
Db 241 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVEDSDVKWVDVSNQTS 295
QY 190 FKILSLHFGQKYLVOVRCKP 209
Db 296 CRLAGLKPGETVYFVQVRCP 315

RESULT 3
US-09-736-842-2
; Sequence 2, Application US/09736842
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: Novel Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/736,842
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: US/09/120,601
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/012,072
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-736-842-2

Query Match      25.0%; Score 292; DB 5; Length 405;
Best Local Similarity 38.0%; Pred. No. 4.3e-20;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFNLTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDG--LPTNYSLTYYHREGETLM 72
Db 106 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGD 164

; APPLICANT: Hermann, Klaus
; APPLICANT: Heiden, Esmeralda
; APPLICANT: Pilarzsky, Christian
; APPLICANT: Brummendorf, Thomas
; APPLICANT: Staub, Eike
; APPLICANT: Ropcke, Stefan
; APPLICANT: Mennerich, Detlev
; APPLICANT: Kinnemann, Henrik
; APPLICANT: Li, Xinzhang
; TITLE OF INVENTION: Human nucleic acid sequences from lung tumours
; FILE REFERENCE: 00154/002001
; CURRENT APPLICATION NUMBER: US/10/821,801
; CURRENT FILING DATE: 2004-04-09
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 794
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-821-801-794

Query Match      25.1%; Score 293; DB 6; Length 422;
Best Local Similarity 37.5%; Pred. No. 3.6e-20;
Matches 75; Conservative 28; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFNLTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDG--LPTNYSLTYYHREGETLM 72
Db 123 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGD 181
QY 73 HECPDYITGGPNSCHFGKQYTSWRTYIMMVNAT-QMGSSFSDELYVDVTVIYQDPDPLE 131
Db 182 NTCEEYHTVGPHSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPPD 240
QY 132 LAV-EVKQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKEPEKAAWE-IHFAGQOTE 189
Db 241 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVEDSDVKWVDVSNQTS 295
QY 190 FKILSLHFGQKYLVOVRCKP 209
Db 296 CRLAGLKPGETVYFVQVRCP 315

RESULT 3
US-09-736-842-2
; Sequence 2, Application US/09736842
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: Novel Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/736,842
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: US/09/120,601
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/012,072
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-736-842-2

Query Match      25.0%; Score 292; DB 5; Length 405;
Best Local Similarity 38.0%; Pred. No. 4.3e-20;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFNLTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDG--LPTNYSLTYYHREGETLM 72
Db 106 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGD 164

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; ORGANISM: Mus musculus  
US-10-603-151-2  
Query Match 25.0%; Score 292; DB 6; Length 425;  
Best Local Similarity 38.0%; Pred. No. 4.6e-20;  
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;  
QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKEFTTCWRPCTDGG--LPTNYSILTYHREGETLM 72  
DB 126 ILAGSCLYVG-LPPEKPNISCSWKNKDLTCRTWTPGAGHETFLHTNYSILKYKLRWYQD 184  
QY 73 HECPDYITGPNCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVDVTVYVQDPPLE 131  
DB 185 NTCEEYHTVGHPSCHIPKD-LALFTPEIWEATNRLGSARSDVLTLDVLDVTTDPPD 243  
QY 132 LAV-EVKQEDRKPYLWIKWSPTLIDLTGFTLLYEIRLKEKAAWE-IHFAGQOTE 189  
DB 244 VHSRVGGLEDQLSVRWV--SPALKDF---LFQAKYQIRYVEDSVKWKVDDVSNQTS 298  
QY 190 FKILSLHPGQKYLVOVRCKP 209  
DB 299 CRLAGLKPGTVYFVQVRCNP 318  
RESULT 6  
US-09-736-842-4  
; Sequence 4, Application US/09736842  
; GENERAL INFORMATION:  
; APPLICANT: Maslakowski, Piotr  
; TITLE OF INVENTION: Novel Orphan Receptors  
; FILE REFERENCE: REG 630  
; CURRENT APPLICATION NUMBER: US/09/736,842  
; PRIOR FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: US/09/120,601  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/012,072  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 434  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-736-842-4  
Query Match 23.4%; Score 273; DB 5; Length 434;  
Best Local Similarity 33.8%; Pred. No. 3e-18;  
Matches 75; Conservative 28; Mismatches 85; Indels 34; Gaps 9;  
QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKEFTTCWRPCTDGG--LPTNYSILTYHREGETLM 72  
DB 109 ILAGSCLYVG-LPPEKPNISCSWKNKDLTCRTWTPGAGHETFLHTNYSILKYKLRWYQD 167  
QY 73 HECPDYITGPNCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVDVTVYVQDPPLE 121  
DB 168 NTCEEYHTVGHPSCHIPKD-LALFTPEIWEATNRLGSARSDVLTLDVLDVTTDPPD 226  
QY 122 -----YIVQDPPLELAV-EVKQEDRKPYLWIKWSPTLIDLTGFTLLYEIRLKEKAAWE-IHFAGQOTE 168  
DB 227 PATPGLSLLVRGKVTTDPPDPVHVSRVGGLEDQLSVRWV--SPALKDF---LFQAKYQ 281  
QY 169 IRLKPEKAAWE-IHFAGQOTEFKILSLHPGQKYLVOVRCKP 209  
DB 282 IRYVEDSVKWKVDDVSNQTSRLAGLKPGTVYFVQVRCNP 323  
RESULT 7  
US-09-736-842-6  
; Sequence 6, Application US/09736842  
; GENERAL INFORMATION:  
; APPLICANT: Maslakowski, Piotr  
; TITLE OF INVENTION: Novel Orphan Receptors  
; FILE REFERENCE: REG 630

; CURRENT APPLICATION NUMBER: US/09/736,842  
; CURRENT FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: US/09/120,601  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/012,072  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-736-842-6  
Query Match 23.4%; Score 273; DB 5; Length 448;  
Best Local Similarity 33.8%; Pred. No. 3.1e-18;  
Matches 75; Conservative 28; Mismatches 85; Indels 34; Gaps 9;  
QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKEFTTCWRPCTDGG--LPTNYSILTYHREGETLM 72  
DB 123 ILAGSCLYVG-LPPEKPNISCSWKNKDLTCRTWTPGAGHETFLHTNYSILKYKLRWYQD 181  
QY 73 HECPDYITGPNCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVDVTVYVQDPPLE 121  
DB 182 NTCEEYHTVGHPSCHIPKD-LALFTPEIWEATNRLGSARSDVLTLDVLDVTTDPPD 240  
QY 122 -----YIVQDPPLELAV-EVKQEDRKPYLWIKWSPTLIDLTGFTLLYEIRLKEKAAWE-IHFAGQOTE 168  
DB 241 PATPGLSLLVRGKVTTDPPDPVHVSRVGGLEDQLSVRWV--SPALKDF---LFQAKYQ 295  
QY 169 IRLKPEKAAWE-IHFAGQOTEFKILSLHPGQKYLVOVRCKP 209  
DB 296 IRYVEDSVKWKVDDVSNQTSRLAGLKPGTVYFVQVRCNP 337  
RESULT 8  
US-10-806-655-4  
; Sequence 4, Application US/10806655  
; GENERAL INFORMATION:  
; APPLICANT: Sundstrom, Michael  
; TITLE OF INVENTION: Modified Cytokine Receptor Protein  
; FILE REFERENCE: 31611-8A  
; CURRENT APPLICATION NUMBER: US/10/806,655  
; CURRENT FILING DATE: 2004-03-23  
; PRIOR APPLICATION NUMBER: US 09/355664  
; PRIOR FILING DATE: 1999-10-08  
; PRIOR APPLICATION NUMBER: PCT/SE98/00277  
; PRIOR FILING DATE: 1998-02-17  
; PRIOR APPLICATION NUMBER: SE 9700566 4  
; PRIOR FILING DATE: 1997-02-18  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 4  
; LENGTH: 202  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-806-655-4  
Query Match 22.5%; Score 262.5; DB 6; Length 202;  
Best Local Similarity 31.0%; Pred. No. 1.2e-17;  
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;  
QY 30 KPEIFKCRSPNKEFTTCWRW---RPGTD--GGLPTNYSILTYHREGETLMHECPDYITGCP 83  
DB 19 EPKFTKCRSPERETFSCHWTDEVHGTNKLQFIQLFYTRNTQEWQEKCPDVSAGE 78  
QY 84 NSCHFGKQYTSWRTYIMVNATOMGSSFSDELYVDVTVYVQDPPLELAVVEVQKPEDRK 143  
DB 79 NSCYNSSFSTIWIPIY--CIKLTNSGGTV-DEKCFSDVEIVQDPPPIALN----- 125  
QY 144 PYLW-----IKWSPPTLIDLTGFTLLYEIRLKEKAAWEIHFAGQOT 188

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Db 126 ---WTLNVLSTGIHADIQVRWEAPRNADIQKGMVLEVELOQYKEVNETKWKMDPILTT 182
QY 189 EFKILSLHPGQKYLIVQVRCK 208
Db 183 SVFVSLKVDKEYEVRVRSK 202

RESULT 9
US-10-806-655-3
; Sequence 3, Application US/10806655
; GENERAL INFORMATION:
; APPLICANT: Sundstrom, Michael
; APPLICANT: Norstedt, Gunnar
; TITLE OF INVENTION: Modified Cytokine Receptor Protein
; FILE REFERENCE: 31611-8A
; CURRENT APPLICATION NUMBER: US/10/806,655
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US 09/355664
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: PCT/SE98/00277
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: SE 9700566 4
; PRIOR FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-806-655-3

Query Match 22.5%; Score 262.5; DB 6; Length 203;
Best Local Similarity 31.0%; Pred. No. 1.2e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKETFTTCW-----RPGTD--GGLPNTYSLTYHREGTLMHCECPDYITGGP 83
Db 19 EPKFTKCRSPERETFSCHWTDEVHHGTKNLGPIQLFYTRNTQEWTKQWKECPDYVSAGE 78
QY 84 NSCHFGQYTSWVRTYIMVNATQMGSSFSDELVDVTVIVQDPPLLEAVEVKQPEDRK 143
Db 79 NSCYFNSFTSIWIPY--CIKLTNSGGTV-DEKCFSDVDEIVQDPPIALN-----125
QY 144 PYLW-----IKWSPPTLIDLKTGWFTLLYVEIRLKPKEAAWEIHFAGQOT 188
Db 126 ---WTLNVLSTGIHADIQVRWEAPRNADIQKGMVLEVELOQYKEVNETKWKMDPILTT 182
QY 189 EFKILSLHPGQKYLIVQVRCK 208
Db 183 SVFVSLKVDKEYEVRVRSK 202

US-10-806-655-1
; Sequence 1, Application US/10806655
; GENERAL INFORMATION:
; APPLICANT: Sundstrom, Michael
; APPLICANT: Norstedt, Gunnar
; TITLE OF INVENTION: Modified Cytokine Receptor Protein
; FILE REFERENCE: 31611-8A
; CURRENT APPLICATION NUMBER: US/10/806,655
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US 09/355664
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: PCT/SE98/00277
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: SE 9700566 4
; PRIOR FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-806-655-1

Query Match 22.5%; Score 262.5; DB 6; Length 237;
Best Local Similarity 31.0%; Pred. No. 1.5e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKETFTTCW-----RPGTD--GGLPNTYSLTYHREGTLMHCECPDYITGGP 83
Db 50 EPKFTKCRSPERETFSCHWTDEVHHGTKNLGPIQLFYTRNTQEWTKQWKECPDYVSAGE 109
QY 84 NSCHFGQYTSWVRTYIMVNATQMGSSFSDELVDVTVIVQDPPLLEAVEVKQPEDRK 143
Db 110 NSCYFNSFTSIWIPY--CIKLTNSGGTV-DEKCFSDVDEIVQDPPIALN-----156
QY 144 PYLW-----IKWSPPTLIDLKTGWFTLLYVEIRLKPKEAAWEIHFAGQOT 188
Db 157 ---WTLNVLSTGIHADIQVRWEAPRNADIQKGMVLEVELOQYKEVNETKWKMDPILTT 213
QY 189 EFKILSLHPGQKYLIVQVRCK 208
Db 214 SVFVSLKVDKEYEVRVRSK 233

RESULT 12
PCT-US04-02188-142
; Sequence 142, Application PC/TUS0402188
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-806-655-2

Query Match 22.5%; Score 262.5; DB 6; Length 206;
Best Local Similarity 31.0%; Pred. No. 1.2e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKETFTTCW-----RPGTD--GGLPNTYSLTYHREGTLMHCECPDYITGGP 83
Db 19 EPKFTKCRSPERETFSCHWTDEVHHGTKNLGPIQLFYTRNTQEWTKQWKECPDYVSAGE 78
QY 84 NSCHFGQYTSWVRTYIMVNATQMGSSFSDELVDVTVIVQDPPLLEAVEVKQPEDRK 143
Db 79 NSCYFNSFTSIWIPY--CIKLTNSGGTV-DEKCFSDVDEIVQDPPIALN-----125
QY 144 PYLW-----IKWSPPTLIDLKTGWFTLLYVEIRLKPKEAAWEIHFAGQOT 188
Db 126 ---WTLNVLSTGIHADIQVRWEAPRNADIQKGMVLEVELOQYKEVNETKWKMDPILTT 182
QY 189 EFKILSLHPGQKYLIVQVRCK 208
Db 183 SVFVSLKVDKEYEVRVRSK 202

RESULT 11
US-10-806-655-1
; Sequence 1, Application US/10806655
; GENERAL INFORMATION:
; APPLICANT: Sundstrom, Michael
; APPLICANT: Norstedt, Gunnar
; TITLE OF INVENTION: Modified Cytokine Receptor Protein
; FILE REFERENCE: 31611-8A
; CURRENT APPLICATION NUMBER: US/10/806,655
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US 09/355664
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: PCT/SE98/00277
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: SE 9700566 4
; PRIOR FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-806-655-1

Query Match 22.5%; Score 262.5; DB 6; Length 237;
Best Local Similarity 31.0%; Pred. No. 1.5e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKETFTTCW-----RPGTD--GGLPNTYSLTYHREGTLMHCECPDYITGGP 83
Db 50 EPKFTKCRSPERETFSCHWTDEVHHGTKNLGPIQLFYTRNTQEWTKQWKECPDYVSAGE 109
QY 84 NSCHFGQYTSWVRTYIMVNATQMGSSFSDELVDVTVIVQDPPLLEAVEVKQPEDRK 143
Db 110 NSCYFNSFTSIWIPY--CIKLTNSGGTV-DEKCFSDVDEIVQDPPIALN-----156
QY 144 PYLW-----IKWSPPTLIDLKTGWFTLLYVEIRLKPKEAAWEIHFAGQOT 188
Db 157 ---WTLNVLSTGIHADIQVRWEAPRNADIQKGMVLEVELOQYKEVNETKWKMDPILTT 213
QY 189 EFKILSLHPGQKYLIVQVRCK 208
Db 214 SVFVSLKVDKEYEVRVRSK 233

RESULT 12
PCT-US04-02188-142
; Sequence 142, Application PC/TUS0402188
; GENERAL INFORMATION:
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; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
; FILE REFERENCE: 5151
; CURRENT APPLICATION NUMBER: PCT/US04/02188
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,582
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-02188-142

Query Match      22.5%; Score 262.5; DB 1; Length 638;
Best Local Similarity 31.0%; Pred. No. 4.8e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKEFTTCW-----RPGTD--GGLPTNYSLTYYHREGTLMHECPDYITGGP 83
Db 50 EPKFTKCRSPERETFSCHWTDEVHHGTXNLGPIQLFYTRRNTQEWTKWKECPDYVSAGE 109
QY 84 NSCHFQKQYTSWRTYIMVNATQMGSSFSDELYVDVTYIVQDPPELEAVEVKQPEDRK 143
Db 110 NSCYFNSSFTSIWIPY--CIKLTSNGGTV-DEKCFVSDEIVQDPPIALN----- 156
QY 144 PYLW-----IKWSPPTLIDLKTGFTLLYRIRLKPKEAAEWEIHFAGQOT 188
Db 157 ---WTLNVS LTGTHADIQVRWEAPRNADIQKGMWVLELYQYKEVNETKWKMDPILTT 213
QY 189 EFKILSLHPGQKYLVOVRCK 208
Db 214 SVPVYSLKVDKEYEVRVRSK 233

; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
; FILE REFERENCE: 5151
; CURRENT APPLICATION NUMBER: PCT/US04/02188
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,582
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-02188-142

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; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
; FILE REFERENCE: 5151
; CURRENT APPLICATION NUMBER: US/10/764,425
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,582
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-425-142

Query Match      22.5%; Score 262.5; DB 6; Length 638;
Best Local Similarity 31.0%; Pred. No. 4.8e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKEFTTCW-----RPGTD--GGLPTNYSLTYYHREGTLMHECPDYITGGP 83
Db 50 EPKFTKCRSPERETFSCHWTDEVHHGTXNLGPIQLFYTRRNTQEWTKWKECPDYVSAGE 109
QY 84 NSCHFQKQYTSWRTYIMVNATQMGSSFSDELYVDVTYIVQDPPELEAVEVKQPEDRK 143
Db 110 NSCYFNSSFTSIWIPY--CIKLTSNGGTV-DEKCFVSDEIVQDPPIALN----- 156

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QY 144 PYLW-----IKWSPPTLIDLKTGFTLLYRIRLKPKEAAEWEIHFAGQOT 188
Db 157 ---WTLNVS LTGTHADIQVRWEAPRNADIQKGMWVLELYQYKEVNETKWKMDPILTT 213
QY 189 EFKILSLHPGQKYLVOVRCK 208
Db 214 SVPVYSLKVDKEYEVRVRSK 233

RESULT 14
US-10-821-801-503
; Sequence 503, Application US/10821801
; GENERAL INFORMATION:
; APPLICANT: Hinzmann, Bernd
; APPLICANT: Rosenthal, Andre
; APPLICANT: Hermann, Klaus
; APPLICANT: Heiden, Esmeralda
; APPLICANT: Pilarsky, Christian
; APPLICANT: Brumendorf, Thomas
; APPLICANT: Staub, Elke
; APPLICANT: Ropcke, Stefan
; APPLICANT: Mennerich, Detlev
; APPLICANT: Kinnemann, Henrik
; APPLICANT: Li, Xinzhong
; TITLE OF INVENTION: Human nucleic acid sequences from lung tumours
; FILE REFERENCE: 00154/002001
; CURRENT APPLICATION NUMBER: US/10/821,801
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: DE 103 16 701.3
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 503
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-821-801-503

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Query Match      22.5%; Score 262.5; DB 6; Length 638;
Best Local Similarity 31.0%; Pred. No. 4.8e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKEFTTCW-----RPGTD--GGLPTNYSLTYYHREGTLMHECPDYITGGP 83
Db 50 EPKFTKCRSPERETFSCHWTDEVHHGTXNLGPIQLFYTRRNTQEWTKWKECPDYVSAGE 109
QY 84 NSCHFQKQYTSWRTYIMVNATQMGSSFSDELYVDVTYIVQDPPELEAVEVKQPEDRK 143
Db 110 NSCYFNSSFTSIWIPY--CIKLTSNGGTV-DEKCFVSDEIVQDPPIALN----- 156
QY 144 PYLW-----IKWSPPTLIDLKTGFTLLYRIRLKPKEAAEWEIHFAGQOT 188
Db 157 ---WTLNVS LTGTHADIQVRWEAPRNADIQKGMWVLELYQYKEVNETKWKMDPILTT 213
QY 189 EFKILSLHPGQKYLVOVRCK 208
Db 214 SVPVYSLKVDKEYEVRVRSK 233

RESULT 15
US-10-659-295-35
; Sequence 35, Application US/10659295
; GENERAL INFORMATION:
; APPLICANT: SCHNEIDER, ARMIN
; APPLICANT: SCHAEBITZ, WOLF-RUEDIGER
; APPLICANT: KOLLMAR, RAINER
; APPLICANT: SCHWAB, STEFAN
; TITLE OF INVENTION: METHODS OF TREATING NEUROLOGICAL CONDITIONS WITH HEMATOPOIETIC G
; FILE REFERENCE: 229530US
; CURRENT APPLICATION NUMBER: US/10/659,295
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/10/331,755

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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:15:21 ; Search time 20 seconds  
(without alignments)  
1010.011 Million cell updates/sec

Title: US-10-029-079-3

Perfect score: 1166  
Sequence: 1 MKENVASATVFTLLFLNTC.....KILSLHGGKYLIVQRKPD 210

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78.\*

- 1: PIR1.\*
- 2: PIR2.\*
- 3: PIR3.\*
- 4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1155.5	99.1	288	B59405	prolactin receptor
2	1155.5	99.1	376	A59405	prolactin receptor
3	1155.5	99.1	622	A40144	prolactin receptor
4	935.5	80.2	616	A30304	prolactin receptor
5	865.5	74.2	581	I45971	prolactin receptor
6	837	71.8	310	A29884	prolactin receptor
7	837	71.8	412	A41070	prolactin receptor
8	837	71.8	610	A36116	prolactin receptor
9	837	69.8	292	I77524	prolactin receptor
10	813.5	69.8	303	I77524	prolactin receptor
11	813.5	69.8	608	I53269	prolactin receptor
12	813.5	69.8	831	JQ1655	prolactin receptor
13	688.5	59.0	830	I50455	prolactin receptor
14	683.5	58.6	630	I51086	prolactin receptor
15	549.5	47.1	630	I51086	prolactin receptor
16	504.5	43.3	150	B34631	prolactin receptor
17	489	41.9	156	A32868	prolactin receptor
18	312	26.8	97	I57699	pseudo-prolactin r
19	296	25.4	608	I32823	somatotropin recep
20	291.5	25.0	279	B32985	somatotropin-bindi
21	291.5	25.0	638	I32156	somatotropin recep
22	290.5	24.9	638	I32156	somatotropin recep
23	289.5	24.8	638	B28176	somatotropin recep
24	278.5	23.9	634	I33339	somatotropin-bindi
25	277.5	23.8	677	I33608	somatotropin recep
26	262.5	22.5	638	I33991	somatotropin recep
27	190.5	16.3	837	A34898	granulocyte colony
28	165	14.2	918	A36337	membrane glycoprot
29	163	14.0	771	B38252	granulocyte colony

30	163	14.0	783	2	JH0329	granulocyte colony
31	163	14.0	863	2	C38252	granulocyte colony
32	160	13.7	432	2	I48343	interleukin-11 rec
33	153	13.1	422	2	I37891	interleukin-11 rec
34	142.5	12.2	51	2	I56840	prolactin receptor
35	138	11.8	917	2	I49699	glycoprotein 130 -
36	134.5	11.5	918	2	A44257	interleukin-6 sign
37	134	11.5	372	1	UHHUCN	ciliary neurotroph
38	133	11.4	362	2	S60614	growth promoting a
39	131	11.2	372	2	I58141	ciliary neurotroph
40	130.5	11.2	348	2	JC7907	common cytokine re
41	124	10.6	440	2	JL0144	interleukin-6 rece
42	124	10.6	460	2	JL0145	interleukin-6 rece
43	120	10.3	805	2	S68441	leptin receptor, s
44	120	10.3	892	2	S68439	leptin receptor, s
45	120	10.3	894	2	S68437	leptin receptor, s

ALIGNMENTS

RESULT 1

B59405  
prolactin receptor short form Sib precursor, breast cancer cells T-47D - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Mar-2002  
C:Accession: B59405; B49400  
R:Hu, Z.Z.; Meng, J.; Durau, M.L., 2001  
J. Biol. Chem. 276, 41086-41094, 2001  
A:Title: Isolation and characterization of two novel forms of the human prolactin recep  
A:Reference number: A59405; MUID:21538812; PMID:11518703  
A:Accession: B59405  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-288 <HU>  
A:Cross-references: GB:AF214012; PIDN:AF214012.1  
R:Hu, Z.Z.  
Submitted to GenBank, December, 1999  
A:Reference number: A49400  
A:Accession: B49400  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-288 <HU2>  
A:Cross-references: GB:AF214012; PIDN:AF214012.1  
C:Comment: This is one of the short forms (Sia and Sib) of the human proactin receptor  
ta-casien gene promoter activation, with Sib more effective than Sia. However, their li  
C:Genetics:  
A:Gene: GDB:PRLR  
A:Cross-references: GDB:I20315; OMIM:176761  
A:Map position: 5p13.3-5p13.1  
C:Superfamily: cytokine receptor homology  
C:Keywords: glycoprotein; transmembrane protein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-288/Product: prolactin receptor, short form Sib #status predicted <MAT>  
F:36-221/Domain: cytokine receptor homology <CRS>  
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match		99.1%	Score 1155.5;	DB 2;	Length 288;
Best Local Similarity		99.5%;	Pred. No. 4.3e-95;		
Matches 210;		Conservative	0;	Mismatches	0;
				Indels	1;
				Gaps	1;
QY	1	MKENVASATVFTLLFLNTCLNGQLPGKPEIFKCRSPNKETFTCWWRPGTGGPTNY	60		
Db	1	MKENVASATVFTLLFLNTCLNGQLPGKPEIFKCRSPNKETFTCWWRPGTGGPTNY	60		
QY	61	SLTYHREGFTLMHECPDYITGGPNSCHFGKQVTSMMRTYIMVNAT-QMGSSFSDELYVD	119		
Db	61	SLTYHREGFTLMHECPDYITGGPNSCHFGKQVTSMMRTYIMVNAT-QMGSSFSDELYVD	120		
QY	120	VTVYVQDPPELAVVEVKQPEDRKPYLWKWSPPFLIDLKTGWFTLLYIRLKPAAEW	179		
Db	121	VTVYVQDPPELAVVEVKQPEDRKPYLWKWSPPFLIDLKTGWFTLLYIRLKPAAEW	180		

QY 180 EHFAGQQTFFKILSLHPGQKYLQVVRCKPD 210  
 |||||  
 Db 181 EHFAGQQTFFKILSLHPGQKYLQVVRCKPD 211

RESULT 2  
 A59405  
 A:Accession: A59405  
 A:Molecule type: mRNA  
 A:Residues: 1-622 <BOU>  
 A:Cross-references: GB:M31661; NID:G190361; PIDN:AAA60174.1; PID:G190362  
 R:Fuh, G.; Wellis, J.A.  
 J. Biol. Chem. 270, 13133-13137, 1995  
 A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li  
 A:Reference number: A57018; MUID:95286597; PMID:7768908  
 A:Accession: A57018  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 25-228, 'AW' <RES>  
 A:Cross-references: GB:S78505; NID:G999114; PIDN:AAB34470.1; PID:G999115  
 C:Genetics:  
 A:Gene: GDB:PRLR  
 A:Cross-references: GDB:120315; OMIM:176761  
 A:Map position: Sp13.3-5p13.1  
 C:Superfamily: cytokine receptor homology  
 C:Keywords: glycoprotein; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-376/Product: prolactin receptor, long form #status predicted <MAT>  
 F:36-221/Domain: cytokine receptor homology <CRS>  
 F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Submitted to GenBank, December, 1999  
 A:Reference number: A49400  
 A:Accession: A49400  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-376 <HU2>  
 A:Cross-references: GB:AF214012; PIDN:AF214012.1  
 R:Hu, Z.Z.  
 J. Biol. Chem. 276, 41086-41094, 2001  
 A:Title: Isolation and characterization of two novel forms of the human prolactin recept  
 A:Reference number: A59405; MUID:21538812; PMID:11518703  
 A:Accession: A59405  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-376 <HU2>  
 A:Cross-references: GB:AF214012; PIDN:AF214012.1  
 C:Comment: This is one of the short forms (Sla and Sib) of the human prolactin receptor  
 eta-casein gene promoter activation, with Sla less effective than Sib. However, their li  
 ted COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expe  
 C:Genetics:  
 A:Gene: GDB:PRLR  
 A:Cross-references: GDB:120315; OMIM:176761  
 A:Map position: Sp13.3-5p13.1  
 C:Superfamily: cytokine receptor homology  
 C:Keywords: glycoprotein; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-376/Product: prolactin receptor, short form Sla #status predicted <MAT>  
 F:36-221/Domain: cytokine receptor homology <CRS>  
 F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.1%; Score 1155.5; DB 2; Length 376;  
 Best Local Similarity 99.5%; Pred. No. 5.8e-95;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLLQGLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 |||||  
 Db 1 MKNVASATVFTLLFLNTCLLQGLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60

QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELVD 119  
 |||||  
 Db 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELVD 120

QY 120 VTYVQDPDPLELAVKQPEDEKPKYLVKWSPTTLDLKTGWFTLLYERLKPEKAAEW 179  
 |||||  
 Db 121 VTYVQDPDPLELAVKQPEDEKPKYLVKWSPTTLDLKTGWFTLLYERLKPEKAAEW 180

QY 180 EHFAGQQTFFKILSLHPGQKYLQVVRCKPD 210  
 |||||  
 Db 181 EHFAGQQTFFKILSLHPGQKYLQVVRCKPD 211

Query Match 99.1%; Score 1155.5; DB 2; Length 376;  
 Best Local Similarity 99.5%; Pred. No. 5.8e-95;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLLQGLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 |||||  
 Db 1 MKNVASATVFTLLFLNTCLLQGLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60

QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELVD 119  
 |||||  
 Db 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELVD 120

QY 120 VTYVQDPDPLELAVKQPEDEKPKYLVKWSPTTLDLKTGWFTLLYERLKPEKAAEW 179  
 |||||  
 Db 121 VTYVQDPDPLELAVKQPEDEKPKYLVKWSPTTLDLKTGWFTLLYERLKPEKAAEW 180

QY 180 EHFAGQQTFFKILSLHPGQKYLQVVRCKPD 210  
 |||||  
 Db 181 EHFAGQQTFFKILSLHPGQKYLQVVRCKPD 211

RESULT 3  
 A40144  
 A:Accession: A40144  
 A:Molecule type: mRNA  
 A:Residues: 1-616 <EDE>  
 A:Cross-references: GB:J04510; NID:G165669; PIDN:AAA31457.1; PID:G165670  
 R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.  
 Int. J. Biochem. 22, 1089-1095, 1990  
 A:Title: Purification and partial sequence of the rabbit mammary gland prolactin recepto  
 A:Reference number: A60380; MUID:91146782; PMID:2289615  
 A:Accession: A60380  
 A:Status: protein  
 A:Residues: 41-58, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108,150-164, 'XX', 167  
 A:Note: the amino end of the mature protein was blocked  
 C:Superfamily: cytokine receptor homology  
 C:Keywords: blocked amino end; glycoprotein; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-616/Product: prolactin receptor 2 #status predicted <MAT>  
 F:36-221/Domain: cytokine receptor homology <CRS>

A:Accession: A40144  
 A:Molecule type: mRNA  
 A:Residues: 1-622 <BOU>  
 A:Cross-references: GB:M31661; NID:G190361; PIDN:AAA60174.1; PID:G190362  
 R:Fuh, G.; Wellis, J.A.  
 J. Biol. Chem. 270, 13133-13137, 1995  
 A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li  
 A:Reference number: A57018; MUID:95286597; PMID:7768908  
 A:Accession: A57018  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 25-228, 'AW' <RES>  
 A:Cross-references: GB:S78505; NID:G999114; PIDN:AAB34470.1; PID:G999115  
 C:Genetics:  
 A:Gene: GDB:PRLR  
 A:Cross-references: GDB:120315; OMIM:176761  
 A:Map position: Sp13.3-5p13.1  
 C:Superfamily: cytokine receptor homology  
 C:Keywords: glycoprotein; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-622/Product: prolactin receptor, long form #status predicted <MAT>  
 F:36-221/Domain: cytokine receptor homology <CRS>  
 F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.1%; Score 1155.5; DB 2; Length 622;  
 Best Local Similarity 99.5%; Pred. No. 1e-94;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLLQGLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 |||||  
 Db 1 MKNVASATVFTLLFLNTCLLQGLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60

QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELVD 119  
 |||||  
 Db 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELVD 120

QY 120 VTYVQDPDPLELAVKQPEDEKPKYLVKWSPTTLDLKTGWFTLLYERLKPEKAAEW 179  
 |||||  
 Db 121 VTYVQDPDPLELAVKQPEDEKPKYLVKWSPTTLDLKTGWFTLLYERLKPEKAAEW 180

QY 180 EHFAGQQTFFKILSLHPGQKYLQVVRCKPD 210  
 |||||  
 Db 181 EHFAGQQTFFKILSLHPGQKYLQVVRCKPD 211

RESULT 4  
 A30304  
 A:Accession: A30304  
 A:Molecule type: mRNA  
 A:Residues: 1-616 <EDE>  
 A:Cross-references: GB:J04510; NID:G165669; PIDN:AAA31457.1; PID:G165670  
 R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.  
 Int. J. Biochem. 22, 1089-1095, 1990  
 A:Title: Purification and partial sequence of the rabbit mammary gland prolactin recepto  
 A:Reference number: A30304; MUID:89194578; PMID:2928321  
 A:Accession: A30304  
 A:Status: protein  
 A:Residues: 1-616 <EDE>  
 A:Cross-references: GB:J04510; NID:G165669; PIDN:AAA31457.1; PID:G165670  
 R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.  
 Int. J. Biochem. 22, 1089-1095, 1990  
 A:Title: Purification and partial sequence of the rabbit mammary gland prolactin recepto  
 A:Reference number: A60380; MUID:91146782; PMID:2289615  
 A:Accession: A60380  
 A:Status: protein  
 A:Residues: 41-58, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108,150-164, 'XX', 167  
 A:Note: the amino end of the mature protein was blocked  
 C:Superfamily: cytokine receptor homology  
 C:Keywords: blocked amino end; glycoprotein; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-616/Product: prolactin receptor 2 #status predicted <MAT>  
 F:36-221/Domain: cytokine receptor homology <CRS>



F:235-258/Domain: transmembrane #status predicted <TM>  
F:59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.2%; Score 935.5; DB 2; Length 616;  
Best Local Similarity 78.7%; Pred. No. 3.5e-75;  
Matches 166; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
Db 1 MKENVASMIVFLLLFLNILLKQSPGPKPFIFKCRSEKETFTCWRRPGADGGLPTNY 60

QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELVD 119  
Db 61 TLTYHKEGETLTHECPDYITGGPNSCYFSGKHTSIWTIITVNATQMGSSVSDRYVD 120

QY 120 VTYIVOPDPLEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGFTLLYIRLKPKEAAEW 179  
Db 121 VTIVPEPPANLTLEVKHEDRKPYLWIKWSPPTLIDLKTGFTLLYIRLKPKEAAEW 180

QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCRKP 210  
Db 181 ETHFAGQOTQFKILSLYPGQKYLQVRCRKP 211

RESULT 5  
I45971  
prolactin receptor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 28-Jul-2000  
C:Accession: I45971  
R:Scott, P.; Kessler, M.A.; Schuler, L.A.  
Mol. Cell. Endocrinol. 89, 47-58, 1992  
A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin  
A:Reference number: I45971; MUID:93246019; PMID:1138725  
A:Accession: I45971  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-581 <SCO>  
A:Cross-references: GB:L02549; NID:g163617; PID:AAA51417.1; PID:g163618  
C:Gene: PRLR  
C:Superfamily: cytokine receptor homology  
F:36-221/Domain: cytokine receptor homology <CRS>

Query Match 74.2%; Score 865.5; DB 2; Length 581;  
Best Local Similarity 70.6%; Pred. No. 5.3e-69;  
Matches 149; Conservative 27; Mismatches 34; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
Db 1 MKENVASRVFILLFLSVLLNGQSPPEKPKLVKCRSPGKETFTCWRRPGADGGLPTNY 60

QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNA-TOMGSSFSDELVD 119  
Db 61 TLTYHKEGETLTHECPDYITGGPNSCYFSGKHTSIWKMYITVNAINQMGISSDPLYVH 120

QY 120 VTYIVOPDPLEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGFTLLYIRLKPKEAAEW 179  
Db 121 VTIVPEPPANLTLEVKHEDRKPYLWIKWSPPTLIDLKTGFTLLYIRLKPKEATDW 180

QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCRKP 210  
Db 181 ETHFLLKQTKIFNLYPGQKYLQVRCRKP 211

RESULT 6  
A29884  
prolactin receptor precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 28-Jul-2000  
C:Accession: A29884  
R:Fourtin, J.M.; Jolicœur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shiota, M.; Banville  
Cell 53, 69-77, 1988

A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth h  
A:Reference number: A29884; MUID:88165059; PMID:2832068  
A:Accession: A29884  
A:Molecule type: mRNA  
A:Residues: 1-310 <BOU>  
A:Cross-references: GB:M19304; NID:g206364; PIDN:AAA41937.1; PID:g206365  
C:Superfamily: cytokine receptor homology  
C:Keywords: transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-310/Product: prolactin receptor #status predicted <MAT>  
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 71.8%; Score 837; DB 2; Length 310;  
Best Local Similarity 72.7%; Pred. No. 8.6e-67;  
Matches 149; Conservative 20; Mismatches 34; Indels 2; Gaps 2;

QY 7 SATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNYSLYHR 66  
Db 3 SALAFVLIV-LNISLLKGQSPGKPEIHKCRSPDKETFTCWRRPGTDGGLPTNYSLYSK 61

QY 67 EGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELVDVTVYVQ 125  
Db 62 EGEKTTYECPDYITGGPNSCFPSKQYTSIWKIYIITVNATQMGSSSDPLYVDVTVYVE 121

QY 126 PDPLEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGFTLLYIRLKPKEAAEWHFAG 185  
Db 122 PEPPNLTLEVKQLKDKKTYLWIKWSPPTITDKTGWFTMEYIRLKPKEABEWHFAG 181

QY 186 QTEFKILSLHPGQKYLQVRCRKP 210  
Db 182 HQTEKVFDELVPQKYLQVRCRKP 206

RESULT 7  
A41070  
prolactin receptor Nb2 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 12-Jun-1992 #sequence\_revision 12-Jun-1992 #text\_change 28-Jul-2000  
C:Accession: A41070; I55417  
R:Ali, S.; Pellsgrini, I.; Kelly, P.A.  
J. Biol. Chem. 266, 20110-20117, 1991  
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolac  
A:Reference number: A41070; MUID:92041834; PMID:1718958  
A:Accession: A41070  
A:Molecule type: mRNA  
A:Residues: 1-412 <ALI>  
A:Cross-references: GB:M74152; NID:g206389; PIDN:AAA41946.1; PID:g206390  
R:O'Neal, K.D.; Yu-Dee, L.Y.  
J. Biol. Chem. 269, 26076-26082, 1994  
A:Title: Differential signal transduction of the short, Nb2, and long prolactin recepto  
A:Reference number: I55417; MUID:95014432; PMID:7929319  
A:Accession: I55417  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-412 <RES>  
A:Cross-references: EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PID:g641964  
A:Experimental source: Nb2-11C cell line  
C:Superfamily: cytokine receptor homology  
C:Keywords: transmembrane protein  
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 71.8%; Score 837; DB 2; Length 412;  
Best Local Similarity 72.7%; Pred. No. 1.2e-66;  
Matches 149; Conservative 20; Mismatches 34; Indels 2; Gaps 2;

QY 7 SATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNYSLYHR 66  
Db 3 SALAFVLIV-LNISLLKGQSPGKPEIHKCRSPDKETFTCWRRPGTDGGLPTNYSLYSK 61

QY 67 EGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELVDVTVYVQ 125  
Db 62 EGEKTTYECPDYITGGPNSCFPSKQYTSIWKIYIITVNATQMGSSSDPLYVDVTVYVE 121

QY 126 PDPLELAVKQPEDRKPYLWIKWSPTLLDLKTGFTLLYRILKPEKAAEWEIHFG 185  
 Db 122 PEPRNLTLVKQLKDKKTYLWVKSPTITDVKTGFTMEYRILKPEEAEWEIHFTG 181

QY 186 QOTEFKILSLHPGQKYLQVRCRKP 210  
 Db 182 HQTKFVFDLYPGQKYLQVTRCKPD 206

RESULT 8  
 A34631  
 lactogen receptor 1 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 13-Jul-1990 #sequence\_revision 09-Oct-1992 #text\_change 28-Jul-2000  
 C:Accession: A34631  
 R:Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.  
 Biochem. Biophys. Res. Commun. 168, 415-422, 1990  
 A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA  
 A:Reference number: A34631; MUID:90241201; PMID:2159291  
 A:Accession: A34631  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-610 <ZHA>  
 A:Cross-references: GB:M34083; NID:G205122; PIDN:AAA9273.1; PID:G205123  
 A:Note: the authors translated the codon GAG for residue 533 as Gly  
 C:Superfamily: cytokine receptor homology  
 F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 71.8%; Score 837; DB 2; Length 610;  
 Best Local Similarity 72.7%; Pred. No. 1.9e-66;  
 Matches 149; Conservative 20; Mismatches 34; Indels 2; Gaps 2;

QY 7 SATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWWRPPTDGLPTNYSLYTHR 66  
 Db 3 SALAFVLV-LNISLLKGQSPGKPEIHKCRSPDKETFTCWWRPPTDGLPTNYSLYTYSK 61

QY 67 EGETLMHECDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTYIVQ 125  
 Db 62 EGKTYTECDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTYIVE 121

QY 126 PDPLELAVKQPEDRKPYLWIKWSPTLLDLKTGFTLLYRILKPEKAAEWEIHFG 185  
 Db 122 PEPRNLTLVKQLKDKKTYLWVKSPTITDVKTGFTMEYRILKPEEAEWEIHFTG 181

QY 186 QOTEFKILSLHPGQKYLQVRCRKP 210  
 Db 182 HQTKFVFDLYPGQKYLQVTRCKPD 206

RESULT 9  
 A36116  
 prolactin receptor 2 precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 28-Jul-2000  
 C:Accession: A36116  
 R:Shirot, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, J.  
 Mol. Endocrinol. 4, 1136-1143, 1990  
 A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.  
 A:Reference number: A36116; MUID:91155946; PMID:2293022  
 A:Accession: A36116  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-610 <SHI>  
 A:Cross-references: GB:M57668; NID:G206366; PIDN:AAA1938.1; PID:G206367; GB:M60728  
 C:Superfamily: cytokine receptor homology  
 F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 71.8%; Score 837; DB 2; Length 610;  
 Best Local Similarity 72.7%; Pred. No. 1.9e-66;  
 Matches 149; Conservative 20; Mismatches 34; Indels 2; Gaps 2;

QY 7 SATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWWRPPTDGLPTNYSLYTHR 66  
 Db 3 SALAFVLV-LNISLLKGQSPGKPEIHKCRSPDKETFTCWWRPPTDGLPTNYSLYTYSK 61

QY 67 EGETLMHECDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTYIVQ 125  
 Db 62 EGKTYTECDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTYIVE 121

QY 126 PDPLELAVKQPEDRKPYLWIKWSPTLLDLKTGFTLLYRILKPEKAAEWEIHFG 185  
 Db 122 PEPRNLTLVKQLKDKKTYLWVKSPTITDVKTGFTMEYRILKPEEAEWEIHFTG 181

QY 186 QOTEFKILSLHPGQKYLQVRCRKP 210  
 Db 182 HQTKFVFDLYPGQKYLQVTRCKPD 206

RESULT 10  
 I77525  
 prolactin receptor precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Jul-2000  
 C:Accession: I77525  
 R:Davis, J.A.; Linzer, D.I.H.  
 Mol. Endocrinol. 3, 674-680, 1989  
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.  
 A:Reference number: I57699; MUID:89261824; PMID:2725531  
 A:Accession: I77525  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-292 <RES>  
 A:Cross-references: GB:M22959; NID:G200481; PIDN:AAA39977.1; PID:G200482  
 C:Superfamily: cytokine receptor homology  
 F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 69.8%; Score 813.5; DB 2; Length 292;  
 Best Local Similarity 69.8%; Pred. No. 9.7e-65;  
 Matches 143; Conservative 25; Mismatches 36; Indels 1; Gaps 1;

QY 7 SATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWWRPPTDGLPTNYSLYTHR 66  
 Db 2 SSALAYMLLVLSISLLGQSPGKPEIHKCRSPDKETFTCWWRPPTDGLPTNYSLYTYSK 61

QY 67 EGETLMHECDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTYIVQ 125  
 Db 62 EGKTYTECDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTYIVE 121

QY 126 PDPLELAVKQPEDRKPYLWIKWSPTLLDLKTGFTLLYRILKPEKAAEWEIHFG 185  
 Db 122 PEPRNLTLVKQLKDKKTYLWVKSPTITDVKTGFTMEYRILKPEEAEWEIHFTG 181

QY 186 QOTEFKILSLHPGQKYLQVRCRKP 210  
 Db 182 HQTKFVFDLYPGQKYLQVTRCKPD 206

RESULT 11  
 I77524  
 prolactin receptor precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Jul-2000  
 C:Accession: I77524  
 R:Davis, J.A.; Linzer, D.I.H.  
 Mol. Endocrinol. 3, 674-680, 1989  
 A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.  
 A:Reference number: I57699; MUID:89261824; PMID:2725531  
 A:Accession: I77524  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-303 <RES>  
 A:Cross-references: GB:M22959; NID:G200479; PIDN:AAA39976.1; PID:G200480  
 C:Superfamily: cytokine receptor homology  
 F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 69.8%; Score 813.5; DB 2; Length 303;

**QY**    186 QOTEEKILSLHPGOKYLIVQVRCKPD 210  
       :|::|||::|  
**Db**    182 HQIQKFVFDLYPGOKYLIVQTRCPD 206  
       :|::|||::|

**RESULT 13**

JQ1655  
prolactin receptor precursor - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 28-Jul-2000  
C:Accession: JQ1655  
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.  
Biochem. Biophys. Res. Commun. 188, 490-496, 1992  
A>Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA s  
A:Reference number: JQ1655; MUID:93075121; PMID:1445292  
A:Accession: JQ1655  
A:Molecule type: mRNA  
A:Residues: 1-831 <TRAN>  
A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849  
A:Experimental source: kidney  
C:Superfamily: cytokine receptor homology  
E:1-23/Domain: signal sequence #status predicted <SIG>  
F:21-831/Product: prolactin receptor #status predicted <MAT>  
F:36-219/Domain: cytokine receptor homology <CRS1>  
F:239-425/Domain: cytokine receptor homology <CRS2>  
F:439-462/Domain: transmembrane #status predicted rmmf  
F:59\_91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cova)

**Query Match**                  59.0%; Score 688.5; DB 2; Length 831;  
**Best Local Similarity**      61.9%; Pred. No. 4.1e-53;  
**Matches 117;** Conservative    32; Mismatches    39; Indels        1; Gaps        1;

**QY**    23 NGQLPPGKPEIFKCRSPNKETFTCWRFPTDGGLPTNYSLTYHREGETLMHECPDYITGG 82  
       ::|||::|:  
**Db**    226 SGQSPPKEPTEIIKCPSPEKFTTCWKKPLDGGHTNTLLYSKEGEQQVVCEPCPYRTAG 285  
       :|::|||::|:

**QY**    83 PNSCHFQGKYTSMTWTYIMYNAT-QMGSSFSDELYVDVTYIVQPDPLELAVEVKORPD 141  
       :|::|||::|:  
**Db**    286 FNSCYFDKKHTSFWTYINITYRATNEMSGNSDDPHYVDVTYIVQPPPNNVTLELKKPIN 345  
       :|::|||::|:

**QY**    142 RKPVLWKWSPTTLDLTGTWFTLLYEIRLKPKAAWEIHFAGOOTCFKLISLHPGQKY 201  
       :|::|||::|:  
**Db**    346 RPYLVLTWSPPPLADRVSGWLTLLEYELRLAPEEGEWEETIFVGQTOYQMFLNPFGKY 405  
       :|::|||::|:

**QY**    202 LVQVRCKPD 210  
       :|::|||::|:  
**Db**    406 IIQHCKPD 414  
       :|::|||::|:

**RESULT 14**

I50455  
prolactin receptor - pigeon  
C:Species: Columba livia (domestic pigeon)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 28-Jul-2000  
C:Accession: I50455  
R.Chen, X.; Horseman, N.D.  
Endocrinology 135, 269-276, 1994  
A>Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor  
A:Reference number: I50455; MUID:94283267; PMID:7516866  
A:Accession: I50455  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-830 <CHB>  
A:Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382  
C:Superfamily: cytokine receptor homology  
F:36-220/Domain: cytokine receptor homology <CRS1>  
F:240-426/Domain: cytokine receptor homology <CRS2>

**Query Match**                  58.6%; Score 683.5; DB 2; Length 830;  
**Best Local Similarity**      61.9%; Pred. No. 1.1e-52;  
**Matches 117;** Conservative    32; Mismatches    39; Indels        1; Gaps        1;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:11:30 ; Search time 17 Seconds  
(without alignments)  
643.220 Million cell updates/sec

Title: US-10-029-079-3

Perfect score: 1166

Sequence: 1 MKENVASATVFILLPLNTC.....KILSLHPGKYLQVQRCPD 210

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1155.5	99.1	622	1	PRLR_HUMAN
2	935.5	80.2	616	1	PRLR_RABIT
3	901.5	77.3	581	1	PRLR_CEREL
4	865.5	74.2	581	1	PRLR_BOVIN
5	863.5	74.1	581	1	PRLR_SHEEP
6	837	71.8	610	1	PRLR_RAT
7	813.5	69.8	608	1	PRLR_MOUSE
8	688.5	59.0	831	1	PRLR_CHICK
9	683.5	58.6	830	1	PRLR_COLLI
10	682	58.5	831	1	PRLR_MELGA
11	549.5	47.1	630	1	PRLR_ORENI
12	299	25.6	611	1	GHR_COLLI
13	296	25.4	608	1	GHR_CHICK
14	291.5	25.0	638	1	GHR_RAT
15	290.5	24.9	634	1	GHR_BOVIN
16	280.5	24.9	638	1	GHR_PIG
17	289.5	24.8	638	1	GHR_RABIT
18	278.5	23.9	634	1	GHR_SHEEP
19	277.5	23.8	650	1	GHR_MOUSE
20	262.5	22.5	638	1	GHR_HUMAN
21	259.5	22.3	638	1	GHR_MACMU
22	190.5	16.3	837	1	GCSE_MOUSE
23	165	14.2	918	1	IL6B_HUMAN
24	163	14.0	836	1	GCSE_HUMAN
25	138	11.5	917	1	IL6B_MOUSE
26	134.5	11.5	918	1	IL6B_RAT
27	134	11.5	372	1	CNTR_HUMAN
28	133	11.4	362	1	CNTR_CHICK
29	131	11.2	372	1	CNTR_RAT
30	127	10.9	1165	1	LEPR_PIG
31	126	10.8	380	1	IL32_HUMAN
32	125	10.7	462	1	IL6A_RAT
33	124	10.6	460	1	IL6A_MOUSE

34	120	10.3	1162	1	LEPR_MOUSE
35	116.5	10.0	467	1	IL6A_PIG
36	115	9.9	1451	1	MIM1_HUMAN
37	113.5	9.7	427	1	IL31_HUMAN
38	113.5	9.7	1162	1	LEPR_RAT
39	109.5	9.4	468	1	IL6A_HUMAN
40	109.5	9.4	468	1	LEPR_HUMAN
41	107	9.2	379	1	CYRG_BOVIN
42	104	8.9	415	1	IL5R_MOUSE
43	103.5	8.9	862	1	IL2S_HUMAN
44	102.5	8.8	507	1	EPOR_MOUSE
45	102.5	8.8	507	1	EPOR_RAT

## ALIGNMENTS

RESULT 1

ID	PRLR_HUMAN	STANDARD	PRT	622 AA.
AC	P16471: Q9BX87;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Prolactin receptor precursor (PRL-R).			
GN	PRLR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=90114212; PubMed=2558309;			
RA	Boutin J.-M., Edery M., Shiota M., Jolicoeur C., Lesueur L.,			
RA	Ali S., Gould D., Djiane J., Kelly P.A.,			
RT	"Identification of a cDNA encoding a long form of prolactin receptor			
RT	in human hepatoma and breast cancer cells.";			
RL	Mol. Endocrinol. 3:1455-1461(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=99182102; PubMed=10084611;			
RA	Hu Z.-Z., Zhuang L., Meng J., Leonidres M., Dufau M.L.;			
RT	"The human prolactin receptor gene structure and alternative promoter			
RT	utilization: the generic promoter hp111 and a novel human promoter			
RT	hp(N).";			
RL	J. Clin. Endocrinol. Metab. 84:1153-1156(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Breast carcinoma;			
RA	Kline J.B., Clevenger C.V.;			
RT	"Characterization of a novel and functional human prolactin receptor			
RT	isoform (delta-S1 PRLr) containing only one extracellular			
RT	fibronectin-like domain.";			
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.			
RX	MEDLINE=95075462; PubMed=7984244;			
RA	Somers W., Ullsch M., de Vos A.M., Kossiakoff A.A.;			
RT	"The X-ray structure of a growth hormone-prolactin receptor complex.";			
RL	Nature 372:478-481(1994).			
CC	-!- FUNCTION: This is a receptor for the anterior pituitary hormone prolactin.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=1;			
CC	isoId=P16471-1; Sequence=Displayed;			
CC	Name=2; Synonyms=Delta-S1;			
CC	isoId=P16471-2; Sequence=VSP 001720;			
CC	-!- SIMILARITY: Belongs to the type I cytokine family of receptors.			
CC	Subfamily 1.			
CC	-!- SIMILARITY: Contains 2 fibronectin type III domains.			
CC	-----			

P48356	mus musculus
O18796	sus scrofa
P32179	homo sapien
P78552	homo sapien
Q62959	rattus norv
P08887	homo sapien
P48357	homo sapien
Q95118	bos taurus
P21183	mus musculus
Q99665	homo sapien
P47553	mus musculus
Q07303	rattus norv

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[illegible]

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DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 616
FT DOMAIN 25 234
FT TRANSMEM 235 258
FT DOMAIN 259 616
FT DOMAIN 124 227
FT DOMAIN 124 227
FT DISULFID 36 46
FT CARBOHYD 59 86
FT CARBOHYD 104 104
FT CARBOHYD 132 132
FT CARBOHYD 132 132
FT STRAND 36 38
FT STRAND 44 46
FT STRAND 50 50
FT STRAND 55 55
FT STRAND 61 65
FT STRAND 73 74
FT STRAND 77 77
FT TURN 83 84
FT STRAND 86 88
FT TURN 91 92
FT STRAND 98 104
FT TURN 109 110
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FT TURN 198 199
FT STRAND 202 209
FT STRAND 222 223
SQ SEQUENCE 616 AA; 68840 MW; 800E3166FEF7108C CRC64;

Query Match 80.2%; Score 935.5; DB 1; Length 616;
Best Local Similarity 78.7%; Pred. No. 5.3e-80;
Matches 166; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

QY 1 MKNVAVATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
DB 1 MKNVAVATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
QY 61 SLTYHREGTLMHECPDYITGGPNCHFGKQVTSWRTYIMMUNA-TQMGSSFSDELVD 119
DB 61 SLTYHREGTLMHECPDYITGGPNCHFGKQVTSWRTYIMMUNA-TQMGSSFSDELVD 119
QY 61 TLTYHKEGETLHECPDYKGTGNTCYFSKXHTSIWLYVTNAINQMGVSSDPLYVD 120
DB 61 TLTYHKEGETLHECPDYKGTGNTCYFSKXHTSIWLYVTNAINQMGVSSDPLYVD 120
QY 120 VTYIVQDPDPLEAVEKQEDRKYPLWIKWSPPTLLDLTKGFTLLYELRLKPKAAEW 179
DB 120 VTYIVQDPDPLEAVEKQEDRKYPLWIKWSPPTLLDLTKGFTLLYELRLKPKAAEW 179
QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCKP 210
DB 180 EHFAGQOTEFKILSLHPGQKYLQVRCKP 210
QY 181 ETHFAGQOTEFKILSLHPGQKYLQVRCKP 211
DB 181 ETHFAGQOTEFKILSLHPGQKYLQVRCKP 211

RESULT 3
PRLR CEREL STANDARD; PRT; 581 AA.
AC Q28235;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

```

```

DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
NCBI_TaxID=9960;
RN [1]
RX MEDLINE=96030711; PubMed=7561644;
RA Clarke L.A., Edey M., Loudon A.S., Randall V.A., Postel-Vinay M.C.,
RA Kelly P.A., Jabbour H.N.;
RT "Expression of the prolactin receptor gene during the breeding and
RT non-breeding seasons in red deer (Cervus elaphus): evidence for the
RT expression of two forms in the testis.";
RL J. Endocrinol. 146:313-321(1995).
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone
CC prolactin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; X34953; CAA64419.1; -.
CC HSP; P14787; IAN3.
CC InterPro; IPR002996; CRIA.
CC InterPro; IPR008957; FN III-like.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR003528; Hemtopoptn_L_F1.
CC Pfam; PF00041; fn3; 2.
CC SMART; SM00060; FN3; 1.
CC PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 234
FT TRANSMEM 235 258
FT DOMAIN 259 581
FT DOMAIN 25 122
FT DOMAIN 123 227
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 132 132
FT CARBOHYD 233 233
SQ SEQUENCE 581 AA; 65159 MW; 975E47CB63CF28EC CRC64;

Query Match 77.3%; Score 901.5; DB 1; Length 581;
Best Local Similarity 74.4%; Pred. No. 7.7e-77;
Matches 157; Conservative 24; Mismatches 29; Indels 1; Gaps 1;

QY 1 MKNVAVATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
DB 1 MKNVAVATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
QY 61 SLTYHREGTLMHECPDYITGGPNCHFGKQVTSWRTYIMMUNA-TQMGSSFSDELVD 119
DB 61 SLTYHREGTLMHECPDYITGGPNCHFGKQVTSWRTYIMMUNA-TQMGSSFSDELVD 119
QY 120 VTYIVQDPDPLEAVEKQEDRKYPLWIKWSPPTLLDLTKGFTLLYELRLKPKAAEW 179
DB 120 VTYIVQDPDPLEAVEKQEDRKYPLWIKWSPPTLLDLTKGFTLLYELRLKPKAAEW 179
QY 121 VTYIVEPEPPANLTLEKHPEDRKYPLWIKWSPPTLLDLTKGFTLLYELRLKPKAAEW 180
DB 121 VTYIVEPEPPANLTLEKHPEDRKYPLWIKWSPPTLLDLTKGFTLLYELRLKPKAAEW 180

```

QY 180 EIHFAQGTQFKILSLHPGQKYLVOVRCKPD 210  
 Db 181 EIHFAQGTQKILSLHPGQKYLVOVRCKPD 211

RESULT 4

PRLR\_BOVIN STANDARD; PRT: 581 AA.  
 AC Q28172; Q18880; Q46591;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R).  
 GN PRLR.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG).  
 RC TISSUE=Endometrium;  
 RX MEDLINE=93246019; PubMed=1338725;  
 RA Scott P., Kessler M.A., Schuler L.A.;  
 RT "Molecular cloning of the bovine prolactin receptor and distribution  
 of prolactin and growth hormone receptor transcripts in fetal and  
 utero-placental tissues.";  
 RL Mol. Cell. Endocrinol. 89:47-58(1992).  
 [2]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND TISSUE SPECIFICITY.  
 RC TISSUE=Endometrium;  
 RX MEDLINE=97375450; PubMed=9231767;  
 RA Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;  
 RT "Prolactin receptor heterogeneity in bovine fetal and maternal  
 tissues.";  
 RL Endocrinology 138:3187-3194(1997).  
 [3]  
 RN SEQUENCE OF 25-234 FROM N.A., AND SEQUENCE OF 25-33.  
 RP TISSUE=Mammary gland;  
 RX MEDLINE=95256770; PubMed=7738463;  
 RA Tchelet A., Statten N.R., Krivi G.G., Gertler A.;  
 RT "Extracellular domain of prolactin receptor from bovine mammary gland:  
 expression in Escherichia coli, purification and characterization of  
 its interaction with lactogenic hormones.";  
 RL J. Endocrinol. 144:393-403(1995).  
 [4]  
 RN ALTERNATIVE SPLICING.  
 RP MEDLINE=98001468; PubMed=9343303;  
 RA Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;  
 RT "Long and short forms of the ovine prolactin receptor: cDNA cloning  
 and genomic analysis reveal that the two forms arise by different  
 alternative splicing mechanisms in ruminants and in rodents.";  
 RL J. Mol. Endocrinol. 19:109-120(1997).  
 CC -1- FUNCTION: This is a receptor for the anterior pituitary hormone  
 prolactin.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Long;  
 CC IsoId=Q28172-1; Sequence=Displayed;  
 CC Name=Short;  
 CC IsoId=Q28172-2; Sequence=VSP\_001718, VSP\_001719;  
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues examined; liver,  
 CC peripheral blood lymphocytes, endometrium, corpus luteum,  
 CC intestine, fetal thymus, fetal spleen, fetal liver and fetal  
 CC brain.  
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily 1.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -----  
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 or send an email to license@isb-sib.ch).  
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 CC DR EMBL; LO2549; AAB51417.1; -;  
 CC DR EMBL; AF027403; AAB83999.1; -;  
 CC DR EMBL; AF042780; AAB97748.1; -;  
 CC DR EMBL; AF042780; AAB97747.1; ALT\_SEQ.  
 CC PIR; I45971; I45971.  
 CC HSP; P14787; IAN3.  
 CC InterPro; IPR002996; CRIA.  
 CC InterPro; IPR008957; FN\_III-like.  
 CC InterPro; IPR003961; FN\_III.  
 CC Pfam; PF00041; fn3; 2.  
 CC SMART; SM00060; FN3; 2.  
 CC PROSITE; PS01352; HEMATOPO REC\_L\_F1; 1.  
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing.  
 FT SIGNAL 1 24 PROBABLE.  
 FT CHAIN 25 581 PROLACTIN RECEPTOR.  
 FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 238 258 POTENTIAL.  
 FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 123 227 FIBRONECTIN TYPE-III 2.  
 FT DISULFID 36 46 BY SIMILARITY.  
 FT DISULFID 75 86 BY SIMILARITY.  
 FT CARBOHYD 59 59 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 132 132 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT VARSPLIC 286 296 KGKSEELLRAL -> ISQPSRLVSMF (in isoform  
 Short).  
 FT VARSPLIC 297 581 /FTID=VSP\_001718.  
 FT Missing (in isoform Short).  
 FT /FTID=VSP\_001719.  
 FT CONFLICT 120 120 H -> D (IN REF. 3).  
 FT CONFLICT 128 128 E -> D (IN REF. 3).  
 FT CONFLICT 137 137 L -> V (IN REF. 3).  
 FT CONFLICT 141 141 E -> H (IN REF. 3).  
 FT CONFLICT 156 157 MT -> IM (IN REF. 3).  
 FT CONFLICT 186 186 L -> P (IN REF. 3).  
 SQ SEQUENCE 581 AA; 65153 MW; 7385C0D6956EE139 CRC64;  
 Query Match 74.2%; Score 865.5; DB 1; Length 581;  
 Best Local Similarity 70.6%; Pred. No. 1.8e-73;  
 Matches 149; Conservative 27; Mismatches 34; Indels 1; Gaps 1;  
 QY 1 MKNVASATVFTLLFLNLTCLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNY 60  
 Db 1 MKNAAARVVFIILLFLSVLLNGSQSPPEKPKLVKCRSPKGTFTCWWRPGTGGGLPTNY 60  
 QY 61 SLTVHREGTELMHECPDYITGGNSCHFGKQVTSMTVTYIMVNA-TOMGSSFSDELYVD 119  
 Db 61 TLTVHKEGTILHECPDYKTTGGNSCVFSKKTISIKWYVITVNAINQMGISSDPLYVH 120  
 QY 120 VTIYVQDPPELEAVEVQKQEDRPKPYLWIKWSPTTIDLTGWTFTLLYIRLKPXAAEW 179  
 Db 121 VTIVEPEPPANLTLELKHEDRKPYLWIKWSPTTIDLTGWTFTLLYIRLKPXATDW 180  
 QY 180 EIHFAQGTQFKILSLHPGQKYLVOVRCKPD 210  
 Db 181 EHTFTLKQTKILFNLPGQKYLVOVRCKPD 211

RESULT 5

PRLR\_SHEEP STANDARD; PRT: 581 AA.  
 AC Q46591; Q46569; Q46573; Q46574; P79203; P79205;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R) (OPR).



GN PRLR.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC TISSUE=Liver, and Mammary gland;  
RX MEDLINE=98001468; PubMed=9343303;  
RA Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;  
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning  
RT and genomic analysis reveal that the two forms arise by different  
RT alternative splicing mechanisms in ruminants and in rodents.";  
RL J. Mol. Endocrinol. 19:109-120(1997).  
RN [2]  
RP SEQUENCE OF 61-395 FROM N.A., ALTERNATIVE SPLICING, AND TISSUE  
RP SPECIFICITY.  
RC STRAIN=Scottish Blackface; TISSUE=Anterior pituitary;  
RX MEDLINE=99049302; PubMed=9832462;  
RA Tortorese D.J., Brooks J., Ingleton P.M., McNeilly A.S.;  
RT "Detection of prolactin receptor gene expression in the sheep  
RT pituitary gland and visualization of the specific translation of the  
RT signal in gonadotrophs.";  
RL Endocrinology 139:5215-5223(1998).  
RN [3]  
RP SEQUENCE OF 147-302 FROM N.A., ALTERNATIVE SPLICING, AND TISSUE  
RP SPECIFICITY.  
RC TISSUE=Corpus luteum, and Fetal liver;  
RA Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.;  
RT "Two forms of the prolactin receptor messenger ribonucleic acid are  
RT present in ovine fetal liver and adult ovary.";  
RL Endocrine 3:291-295(1995).  
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone  
CC Prolactin.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=1; Synonyms=Long, L-OPR;  
CC IsoId=O46561-1; Sequence=Displayed;  
CC Name=2; Synonyms=Short, S-OPR;  
CC IsoId=O46561-2; Sequence=VSP\_001732, VSP\_001733;  
CC Name=3; Synonyms=Soluble;  
CC IsoId=O46561-3; Sequence=VSP\_001730, VSP\_001731;  
CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined; liver,  
CC pituitary, adrenal gland, ovary and fetal liver.  
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
CC Subfamily 1.  
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
CC -----  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL; AF041257; AAB96795.1; -;  
DR EMBL; AF041977; AAB96920.1; -;  
DR EMBL; AF041979; AAB97082.1; -;  
DR EMBL; AF042358; AAB97744.1; -;  
DR EMBL; AF042358; AAB97743.1; -;  
DR EMBL; AF041978; AAB96965.1; -;  
DR EMBL; Y10578; CAA71597.1; -;  
DR EMBL; Y10808; CAA71766.1; -;  
DR HSSP; P14787; 1AN3.  
DR InterPro; IPR002396; CRIA.  
DR InterPro; IPR008957; FN.III-like.  
DR InterPro; IPR003961; FN.III.  
DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 2.

DR PROSITE: PS01352; HEMATOPO REC L\_F1; 1.  
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
KW Alternative splicing.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 581 PROLACTIN RECEPTOR.  
FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 238 258 POTENTIAL.  
FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 125 122 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 123 227 FIBRONECTIN TYPE-III 2.  
FT DISULFID 36 46 BY SIMILARITY.  
FT DISULFID 75 86 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 59 59 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 132 132 GOSPEPEKLIKCSPGKETCTCWEPGADGGLPTNYLT  
FT VARSPLIC 24 66 RK -> ASLVVPGKCSVCTYMAVFFVGGIFLHMYLCVDQ  
FT YLLITVTS (in isoform 3).  
FT /FTID=VSP\_001730.  
FT Missing (in isoform 3).  
FT /FTID=VSP\_001731.  
FT KKGSEELLRAL -> ISQPSRLVSF (in isoform  
FT 2).  
FT /FTID=VSP\_001732.  
FT Missing (in isoform 2).  
FT /FTID=VSP\_001733.  
FT I -> V (in REF. 1; AAB97743/AAB97744).  
FT CONFLICT 281 387 E -> K (in REF. 2).  
FT SEQUENCE 581 AA; 65235 MW; EC534FDE538837A0 CRC64;  
SQ  
Query Match 74.1%; Score 863.5; DB 1; Length 581;  
Best Local Similarity 70.6%; Pred. No. 2.8e-73;  
Matches 149; Conservative 28; Mismatches 33; Indels 1; Gaps 1;  
QY 1 MKENVASATVFTLLFLNTCLNGQLPGKPEIFKCRSPNKETFTCWWRPGDGLPTNY 60  
DB 1 MKENASRVLFILLFLFASLLNGQSPPEKPKLIKCRSPGKETFTCWWRPGADGLPTNY 60  
QY 61 SLTYHREGTLMHECPDYITGPNNSCHFGKQYTSWRTYIMVMA-TOMGSSFSDELVD 119  
DB 61 TLTYRKEGTLMHECPDYKGTGPNNSCYFSKYTSWKWYIVITVSAINQVSSDPLVD 120  
QY 120 VTYIVQDPPLLEAVEVQPEKPEYLMKWSPPILDLKTGWFTLLYEIRLKPEAAEW 179  
DB 121 VTYIVPEPPVNLTLKHPEDRKYLKWSPPILTDVKSGWFSIQYIEIRLKPEKATDW 180  
QY 180 EHPAGQQTFFKLSLHPGQKYLQVRCKP 210  
DB 181 ETHFAPKLTQLKIFNLPGQKYLQVRCKP 211  
RESULT 6  
ID PRLR\_RAT STANDARD; PRT; 610 AA.  
AC P05710; Q62832; Q63451; Q63479; Q63723; Q64274;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Prolactin receptor precursor (PRL-R) (lactogen receptor).  
GN PRLR.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=91155946; PubMed=2293022;  
RA Shiota M., Banville D., Ali S., Jolicoeur C., Boutin J.M.,  
RA Edery M., Djiane J., Kelly P.A.;  
RT "Expression of two forms of prolactin receptor in rat ovary and  
RT liver".  
RL Mol. Endocrinol. 4:1136-1143(1990).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC STRAIN=Sprague-Dawley; TISSUE=Ovary;  
 RX MEDLINE=90241201; PubMed=2159291;  
 RA Zhang R., Buczko E., Tsai-Morris C.-H., Hu Z.Z., Dufau M.L.;  
 RT "Isolation and characterization of two novel rat ovarian lactogen  
 RL receptor cDNA species";  
 RL Biochem. Biophys. Res. Commun. 168:415-422(1990).  
 RN [3]  
 RP SEQUENCE OF 281-610 FROM N.A.  
 RA Banville D., Stocco R., Murthy K.K., Boie Y., Kelly P.A.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=88165059; PubMed=2832068;  
 RA Boutin J.-M., Jolicoeur C., Okamura H., Gagnon J., Edery M.,  
 RA Shirota M., Banville D., Dusanter-Fourt I., Djiane J., Kelly P.A.;  
 RT "Cloning and expression of the rat prolactin receptor, a member of  
 RL the growth hormone/prolactin receptor gene family";  
 RL Cell 53:69-77(1988).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RC TISSUE=Lymphoma;  
 RX MEDLINE=92041834; PubMed=1718958;  
 RA Ali S., Pelligrini I., Kelly P.A.;  
 RT "A prolactin-dependent immune cell line (Nb2) expresses a mutant form  
 RL of prolactin receptor";  
 RL J. Biol. Chem. 266:20110-20117(1991).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RX MEDLINE=95014432; PubMed=7929319;  
 RA O'Neal K.D., Yu-Lee L.Y.;  
 RT "Differential signal transduction of the short, Nb2, and long  
 RL prolactin receptors. Activation of interferon regulatory factor-1 and  
 RL cell proliferation";  
 RL J. Biol. Chem. 269:26076-26082(1994).  
 CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone  
 prolactin.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=Long;  
 CC IsoId=P05710-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Short;  
 CC IsoId=P05710-2; Sequence=VSP\_001725, VSP\_001726;  
 CC Name=3; Synonyms=Medium;  
 CC IsoId=P05710-3; Sequence=VSP\_001727, VSP\_001728;  
 CC Name=4; Synonyms=Nb2;  
 CC IsoId=P05710-4; Sequence=VSP\_001729;  
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily 1.  
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
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 CC -----  
 CC DR EMBL; M57668; AAA41938.1; -  
 CC DR EMBL; M34083; AAA79273.1; -  
 CC DR EMBL; L48060; AAA79274.1; -  
 CC DR EMBL; U34730; AAA32053.1; -  
 CC DR EMBL; M19304; AAA41937.1; -  
 CC DR EMBL; M74152; AAA41946.1; -  
 CC DR EMBL; U07567; AAA61784.1; -  
 CC DR PIR; A29884; A29884.  
 CC DR PIR; A34631; A34631.  
 CC DR PIR; A36116; A36116.  
 CC DR PIR; A41070; A41070.  
 CC DR PIR; B34631; B34631.  
 CC DR PDB; 1F6F; 20-DEC-00.

DR InterPro; IPR002996; CRIA.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003288; Hemopoptn\_L\_F1.  
 DR Pfam; PF00041; fn3; 2.  
 DR SMART; SM00060; FN3; 2.  
 DR PROSITE; PS01352; HEMATOPO REC L\_F1; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing; 3D-structure.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 610 PROLACTIN RECEPTOR.  
 FT DOMAIN 20 229 EXTRACELLULAR (BY SIMILARITY).  
 FT TRANSMEM 230 253 BY SIMILARITY.  
 FT DOMAIN 254 610 CYTOPLASMIC (BY SIMILARITY).  
 FT DOMAIN 20 117 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 119 222 FIBRONECTIN TYPE-III 2.  
 FT DISULFID 31 41 BY SIMILARITY.  
 FT DISULFID 70 81 BY SIMILARITY.  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .).  
 FT VARSPLIC 131 150 EVKQKDKTKTYLWKWSPT -> DYRWEVSHQEQALPKSA  
 FT VARSPLIC 151 610 /FTid=VSP\_001725.  
 FT VARSPLIC 281 310 Missing (in isoform 2).  
 FT VARSPLIC 311 610 /FTid=VSP\_001726.  
 FT VARSPLIC 342 539 Missing (in isoform 3).  
 FT CONFLICT 236 236 Missing (in isoform 4).  
 FT CONFLICT 345 345 V -> A (IN REF. 2).  
 FT CONFLICT 465 465 G -> V (IN REF. 2).  
 FT CONFLICT 466 466 E -> K (IN REF. 1).  
 FT CONFLICT 469 469 Q -> E (IN REF. 2).  
 FT CONFLICT 541 541 A -> G (IN REF. 2).  
 FT CONFLICT 555 555 T -> M (IN REF. 1).  
 FT CONFLICT 555 555 Q -> K (IN REF. 2).  
 SQ SEQUENCE 610 AA; 68599 MW; 83D04D832861295D CRC64;  
 Query Match 71.8%; Score 837; DB 1; Length 610;  
 Best Local Similarity 72.7%; Pred. No. 9e-71;  
 Matches 149; Conservative 20; Mismatches 34; Indels 2; Gaps 2;  
 QY 7 SATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLYYR 66  
 DB 3 SALAFVLLV-LNISLLKGQSPGKPEIFKCRSPDKETFTCWWRPGTDGGLPTNYSLYSK 61  
 QY 67 EGETLMECEPDYITGGPNSCHFGKQYTSWMTYIMVNAT-OMGSSFSDELVDVTVYQ 125  
 DB 62 EGETTYCEDYKTSGNCSFFSKQYTSIWKIYITVNATNQMGSSSDPLYVDVTVIVE 121  
 QY 126 PDPELEAVEVKQPEDRKPYLWKWSPTLIDLTGNTFLYIRLKPEKAAEWEHFFAG 185  
 DB 122 PEPRNLTLSEVKQLDKKTKTYLWKWSPTTIDVKTGTFMEYIRLKPEAEWEHFFTG 181  
 QY 186 QQTEFKLSLHFGQKYLQVQCKPD 210  
 DB 182 HQIQKRVFDLYPGQKYLQVQCKPD 206  
 RESULT 7  
 PRLR MOUSE  
 ID\_PRLR\_MOUSE STANDARD; PRT; 508 AA.  
 AC Q08501; P15212; P15213; Q62099;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R).  
 GN PRLR.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A. (ISOFORM PRL-R3).  
 RC STRAIN=C3H; TISSUE=Mammary Gland;  
 RX MEDLINE=94085788; PubMed=8262385;  
 RA Moore R.C., Oka T.;  
 RT "Cloning and sequencing of the cDNA encoding the murine mammary gland  
 RL long-form prolactin receptor.";  
 RL Gene 134:263-265(1993).  
 [2]  
 RP SEQUENCE FROM N.A. (ISOFORM PRL-R3).  
 RC STRAIN=Swiss Webster; TISSUE=Liver;  
 RX MEDLINE=9307149; PubMed=8319571;  
 RA Clarke D.L., Linzer D.I.H.;  
 RT "Changes in prolactin receptor expression during pregnancy in the  
 RL mouse ovary.";  
 RL Endocrinology 133:224-232(1993).  
 [3]  
 RP SEQUENCE FROM N.A. (ISOFORM PRL-R3).  
 RA Sasaki M.;  
 RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A. (ISOFORM PRL-R3).  
 RC STRAIN=BALB/c; TISSUE=Mammary Gland;  
 RA Edery M., Peret A., Nandi S., Kelly P.A.;  
 RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.  
 [5]  
 RP SEQUENCE FROM N.A. (ISOFORMS PRL-R2 AND PRL-R1).  
 RC STRAIN=Swiss Webster; TISSUE=Liver;  
 RX MEDLINE=89261824; PubMed=2725531;  
 RA Davis J.A., Linzer D.I.H.;  
 RT "Expression of multiple forms of the prolactin receptor in mouse  
 RL liver.";  
 RL Mol. Endocrinol. 3:674-680(1989).  
 CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone  
 CC prolactin.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=PRL-R3; Sequence=Displayed;  
 CC IsoId=Q08501-1; Sequence=VSP\_001723, VSP\_001724;  
 CC Name=PRL-R1;  
 CC IsoId=Q08501-2; Sequence=VSP\_001723, VSP\_001722;  
 CC Name=PRL-R2;  
 CC IsoId=Q08501-3; Sequence=VSP\_001721, VSP\_001722;  
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily 1.  
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -----  
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 CC -----  
 CC EMBL; L13593; AAC37641.1; -  
 CC EMBL; L14811; AAA02686.1; -  
 CC EMBL; D10214; BAA01066.1; -  
 CC EMBL; X73372; CAA51789.1; -  
 CC EMBL; M22959; AAA39977.1; -  
 CC EMBL; M22958; AAA39976.1; -  
 CC PIR; I53269; I53269.  
 CC PIR; I7524; I7524.  
 CC PIR; I7525; I7525.  
 CC HSP; P16471; IEP3.  
 CC MGD; MGI:97763; Brk.  
 CC InterPro; IPR002996; CRIA.  
 CC InterPro; IPR008957; FN.III-like.  
 CC InterPro; IPR003961; FN.III.

DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
 DR Pfam; PF00041; FN3.2;  
 DR SMART; SMO0060; FN3.2;  
 DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing.  
 FT SIGNAL 1 19  
 FT CHAIN 20 608  
 FT DOMAIN 20 229  
 FT TRANSMEM 230 253  
 FT DOMAIN 254 608  
 FT DOMAIN 20 117  
 FT DOMAIN 119 222  
 FT DISULFID 31 41  
 FT DISULFID 70 81  
 FT CARBOHYD 54 54  
 FT CARBOHYD 99 99  
 FT CARBOHYD 127 127  
 FT VARSPLIC 281 292  
 FT  
 FT VARSPLIC 293 608  
 FT  
 FT VARSPLIC 281 303  
 FT  
 FT VARSPLIC 304 608  
 FT  
 FT CONFLICT 558 558  
 FT L -> F (IN REF. 2).  
 FT SEQUENCE 608 AA; 68240 MW; B8CE202B2EFC9FC6 CRC64;  
 Query Match 69.8%; Score 813.5; DB 1; Length 608;  
 Best Local Similarity 69.8%; Pred. No. 1.4e-68;  
 Matches 143; Conservative 25; Mismatches 36; Indels 1; Gaps 1;  
 QY 7 SATVFTLLFLNTCLLNGQLPQKPEIKCRSPNKETETCWWRPGTGGGLPTNYSLTYHR 66  
 DB 2 SSALAYMLLVLSILLNGSQSPGKPEIHKCRSPDKETTCWNPQSDGLPTNYSLTYSK 61  
 QY 67 EGETLMHECPDYITGPNNSCHFGKYQTSWRTYIMVNAT-OMGSSFDELYVDVTVYVQ 125  
 DB 62 EGEKNTYECPDYKTSQNSCFESKQYTSWKIYITVNATNEMSGSTSDPLVDVTVYVE 121  
 QY 126 PDPLLEAVEVKQPEDRKYPLWKSPPTLIDKGTWFTLLYEIRLKEKAAEWIHFAG 185  
 DB 122 PEPPNLTLEVKQLDKKTYLWVKLWLPPTITDVKGTWFTMEYELRKSEADEWHFTG 181  
 QY 186 QQTEFKILSLHFGQKYLQVQRCPPD 210  
 DB 182 HQTQFKVFDLPQKYLQVQTRCKPD 206  
 RESULT 8  
 PRLR\_CHICK  
 ID PRLR\_CHICK STANDARD; PRT; 831 AA.  
 AC Q04594;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R) (CPRLP).  
 DE PRLR.  
 OS Gallus gallus (Chicken).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=White Leghorn; TISSUE=Kidney;  
 RX MEDLINE=93075121; PubMed=1445292;  
 RA Tanaka M., Maeda K., Okubo T., Nakashima K.;  
 RT "Double antenna structure of chicken prolactin receptor deduced from  
 RT the cDNA sequence.";

```

RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone
CC prolactin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
CC
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CC -----
CC EMBL; D13154; BAA02439.1; ..
CC PIR; JQ1655; JQ1655.
CC HSSP; P16471; 1BP3.
CC InterPro; IPR002996; CR1A.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003528; Hemtopoptn_L_Fl.
CC Pfam; PF00041; fn3; 4.
CC SMART; SM00060; FN3; 4.
CC PROSITE; PS01352; HEMATOPO REC L_Fl; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
CC SIGNAL 23
CC CHAIN 1 23
CC DOMAIN 24 831
CC TRANSMEM 24 438
CC DOMAIN 439 459
CC DOMAIN 460 831
CC CYTOPLASMIC (POTENTIAL).
CC FIBRONECTIN TYPE-III 1.
CC FIBRONECTIN TYPE-III 2.
CC FIBRONECTIN TYPE-III 3.
CC FIBRONECTIN TYPE-III 4.
CC BY SIMILARITY.
CC CARBOHYD 75 86
CC CARBOHYD 59 59
CC CARBOHYD 91 91
CC CARBOHYD 100 100
CC CARBOHYD 112 112
CC CARBOHYD 132 132
CC CARBOHYD 262 262
CC CARBOHYD 303 303
CC CARBOHYD 315 315
CC CARBOHYD 335 335
CC CARBOHYD 831 AA; 94102 MW; 1C4E75791DCABE9 CRC64;
CC SEQUENCE
CC
CC Query Match 59.0%; Score 688.5; DB 1; Length 831;
CC Best Local Similarity 61.9%; Pred. No. 1.1e-56;
CC Matches 117; Conservative 32; Mismatches 39; Indels 1; Gaps 1;
QY 23 NGOLPFGKEIFKCRSPNKETTCWRRPGTDCGLPTNYSLTTHRGETLMHCEPDYITGG 82
Db 226 SGQSPPEKPTIKCRSPKEKTTTCWKPGDGHPTNTLLYSKGEQVYECPDYRTAG 285
QY 83 PNSCHFGKQYTMWRTYIMMNAAT-QMGSSFSDELVDVYTVIQDPDPLEAVEVKQPED 141
Db 286 PNSCYFDKHTSFTWITNYITVRAATNMGNSSDPHVDVTVYIQDPDPPVNTLELKKPIN 345
QY 142 RPYLWIKSPPTLDLTKTGWNTLYEYRLKPEKAAEWHIHPAGQOTFKLSLHPGQKY 201
Db 346 RPYLVLLTWSPPPLADVRSGWLTLEYELRLKPEEGEWEETTFVGQOTQYKMFSLNPGKY 405
QY 202 LVQVRCKPD 210
Db 406 IIQHCKPD 414

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RESULT 9

PRLR\_COLLI

ID PRLR\_COLLI STANDARD; PRT; 830 AA.

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AC Q0374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OY NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cropsac;
RX MEDLINE=94283267; PubMed=7516866;
RA Chen X., Horseman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin
RT receptor.";
RL Endocrinology 135:269-276(1994).
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone
CC prolactin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
CC
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CC -----
CC EMBL; U07694; AAA20646.1; ..
CC PIR; I50455; I50455.
CC HSSP; P16471; 1BP3.
CC InterPro; IPR002996; CR1A.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003528; Hemtopoptn_L_Fl.
CC Pfam; PF00041; fn3; 4.
CC SMART; SM00060; FN3; 4.
CC PROSITE; PS01352; HEMATOPO REC L_Fl; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
CC SIGNAL 23
CC CHAIN 1 23
CC DOMAIN 24 830
CC TRANSMEM 24 439
CC DOMAIN 440 460
CC CYTOPLASMIC (POTENTIAL).
CC FIBRONECTIN TYPE-III 1.
CC FIBRONECTIN TYPE-III 2.
CC FIBRONECTIN TYPE-III 3.
CC FIBRONECTIN TYPE-III 4.
CC BY SIMILARITY.
CC CARBOHYD 75 86
CC CARBOHYD 59 59
CC CARBOHYD 91 91
CC CARBOHYD 100 100
CC CARBOHYD 112 112
CC CARBOHYD 132 132
CC CARBOHYD 263 263
CC CARBOHYD 304 304
CC CARBOHYD 316 316
CC CARBOHYD 336 336
CC CARBOHYD 830 AA; 94507 MW; 3B074E83CDF69EFF CRC64;
CC SEQUENCE
CC
CC Query Match 58.8%; Score 683.5; DB 1; Length 830;
CC Best Local Similarity 61.9%; Pred. No. 3.1e-56;
CC Matches 117; Conservative 32; Mismatches 39; Indels 1; Gaps 1;
QY 23 NGOLPFGKEIFKCRSPNKETTCWRRPGTDCGLPTNYSLTTHRGETLMHCEPDYITGG 82
Db 227 NGEPSPEKPTIKCRSPKEKTTTCWKPGDGHPTNTLLYSKGEQVYECPDYRTAG 286

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QY 83 PNCSEFGKQYTSWRTYIMVAT-OMGSSFSDELVDVTVYIVQPPPELEAVEKQPED 141  
 DB 287 PNCYCDKHTSWTYITVATNEIGNSVSDPLVDVTVYIVQPPVNTLELKTYN 346  
 QY 142 RKPYLWIKWSPPLDILKGTWFTLLYELIKPKAEWEIHPAGQOTEFKILSLHPGQXY 201  
 DB 347 RKPYLVLTWSPPLADVRSGMLTLDYELRLKPEAEWETIFVGGQTHYKMFSLNPGKXY 406  
 QY 202 LVQVRCKPD 210  
 DB 407 IVQIHCKPD 415  
 RESULT 10  
 PRLR\_MELGA STANDARD; PRT; 831 AA.  
 AC Q1094; Q1091; Q1092;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R) (TPRLR).  
 GN PRLR.  
 OS Meleagris gallopavo (Common turkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.  
 OX NCBI\_TaxID=9103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=8902221;  
 RA Zhou J.F., Zadworny D., Guemene D., Kuhnlein U.,  
 RT "Molecular cloning, tissue distribution, and expression of the  
 RT prolactin receptor during various reproductive states in Meleagris  
 RT gallopavo.";  
 RL Biol. Reprod. 55:1081-1090(1996).  
 RN [2]  
 RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.  
 RC TISSUE=Ovary;  
 RA Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone  
 CC prolactin.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily 1.  
 CC -!- SIMILARITY: Contains 4 fibronectin type III domains.  
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 CC EMBL; L76587; AAB01544.1; -;  
 DR EMBL; U22947; AAB75038.1; -;  
 DR EMBL; U22924; AAB75039.1; -;  
 DR HSBF; F16471; 1BP3.  
 DR InterPro; IPR002996; CRI1A.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
 DR Pfam; PF00041; fn3; 4.  
 DR SMART; SM00060; FN3; 3.  
 DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT CHAIN 24 831 PROLACTIN RECEPTOR.  
 FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 439 459 POTENTIAL.  
 FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 123 225 FIBRONECTIN TYPE-III 3.  
 FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.  
 FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.  
 FT DISULFID 36 46 BY SIMILARITY.  
 FT DISULFID 75 86 BY SIMILARITY.  
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 303 303 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 831 AA; 94394 MW; 220916320F77FACI CRC64;  
 Query Match 58.5%; Score 682; DB 1; Length 831;  
 Best Local Similarity 62.0%; Pred. No. 4.3e-56;  
 Matches 119; Conservative 31; Mismatches 40; Indels 2; Gaps 2;  
 QY 21 LINGQL-PPGKPEIFKCSFNKETCTWVRGDTGGTGLPTNYSLTYHREGETLMHECPDYI 79  
 DB 223 LISGLSPPEKPTTKCSPEKFTCWKPLDGGHPTNYTLTYSKREGGEQVTECPDYR 282  
 QY 80 TGGPNSCHFQKQYTSWRTYIMVAT-OMGSSFSDELVDVTVYIVQPPPELEAVEKQ 138  
 DB 283 TAGPNSCYFDKHTSWTYITVATNEIGNSVSDPLVDVTVYIVQPPVNTLELKT 342  
 QY 139 PEDRKPYLWIKWSPPLDILKGTWFTLLYELIKPKAEWEIHPAGQOTEFKILSLHPG 198  
 DB 343 PINRKPYLWLTWSPPLADVRSGMLTLDYELRLKPEAEWETIFVGGQTHYKMFSLNPG 402  
 QY 199 QKYLQVRCKPD 210  
 DB 403 KKYIVQIHCKPD 414  
 RESULT 11  
 PRLR\_ORENI STANDARD; PRT; 630 AA.  
 AC Q91513;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R).  
 GN PRLR.  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=95320210; PubMed=7597076;  
 RA Sandra O., Sohn F., de Luze A., Prunet P., Edery M., Kelly P.A.;  
 RT "Expression cloning of a cDNA encoding a fish prolactin receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:6037-6041(1995).  
 CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone  
 CC prolactin.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily 1.  
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
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-----
CC CC EMBL; L34783; AAA98997.1; -.
CC CC PIR; I51086; I51086.
CC DR HSSP; P16471; IBP3.
CC DR InterPro; IPR002996; CRIA.
CC DR InterPro; IPR008957; FN III-like.
CC DR InterPro; IPR003961; FN III.
CC DR InterPro; IPR003528; Hemtopoptn_L_F1.
CC DR Pfam; PF00041; fn3; 2.
CC DR SMART; SM00060; FN3; 2.
CC DR PROSITE; PS01352; HEMATOPO REC L_F1; 1.
CC KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
CC FT SIGNAL 1 23
CC FT CHAIN 24 630
CC FT DOMAIN 24 234
CC FT TRANSMEM 235 258
CC FT DOMAIN 259 630
CC FT DOMAIN 124 123
CC FT DOMAIN 124 228
CC FT DISULFID 37 47
CC FT DISULFID 76 87
CC FT CARBOHYD 92 92
CC FT CARBOHYD 101 101
CC SQ SEQUENCE 630 AA; 70810 MW; A451563F3D12979D CRC64;

Query Match 47.1%; Score 549.5; DB 1; Length 630;
Best Local Similarity 54.6%; Pred. No. 8.1e-44;
Matches 101; Conservative 26; Mismatches 55; Indels 3; Gaps 3;

Qy 28 PGKPEIFKCSPNKEHTCWRTGGLTNTVSLYHREGETLMEHCDDYITGGNSCH 87
Db 29 PGKPTTEIKCSPEKETFTYALYRKESGSDVHCEPDYHTAGKNSCF 88
Qy 88 FGQYTSWRTYIMVNNATQ-MGSSPSDELYVDVTYVOPDPLELAVEKQPEDRKPYL 146
Db 89 FNKNNTLIWYSNITVATNALGKTVSDPDIDVTVIOPHPKEKUEVTVMK-DQGWPL 147
Qy 147 WIKWSPTLIDLTGWTLLYELRLKE-KAABWEIHFAQQQTEFKILSLHPGQKYLVOV 205
Db 148 RVSWEPKRAKTRSGMTITLYELRVKLEDESEWHAAGQQQWNI FLSRSGTYLIQV 207
Qy 206 RCKPD 210
Db 208 RCRPD 212

RESULT 12
GHR COLLI STANDARD; PRT; 611 AA.
AC Q30375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).
DE protein).
DE GHR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cheng C.H.K.; Shaw P.C.; Tsim K.W.K.; Lau K.P.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: This is a receptor for pituitary gland growth hormone.
CC -!- FUNCTION: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC -!- SIMILARITY: Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
-----
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-----
CC CC EMBL; U20353; AAA84745.1; -.
CC CC HSSP; F10912; IAXI.
CC DR InterPro; IPR002996; CRIA.
CC DR InterPro; IPR008957; FN III-like.
CC DR InterPro; IPR003961; FN III.
CC DR InterPro; IPR003528; Hemtopoptn_L_F1.
CC DR Pfam; PF00041; fn3; 1.
CC DR SMART; SM00060; FN3; 1.
CC DR PROSITE; PS01352; HEMATOPO REC L_F1; 1.
CC KW Receptor; Transmembrane; Glycoprotein; Signal.
CC FT SIGNAL 1 20
CC FT CHAIN 21 611
CC FT DOMAIN 21 240
CC FT TRANSMEM 241 264
CC FT DOMAIN 265 611
CC FT DOMAIN 119 226
CC FT DISULFID 34 44
CC FT DISULFID 75 86
CC FT DISULFID 100 114
CC FT CARBOHYD 16 16
CC FT CARBOHYD 53 53
CC FT CARBOHYD 89 89
CC FT CARBOHYD 130 130
CC FT CARBOHYD 135 135
CC FT CARBOHYD 174 174
CC SQ SEQUENCE 611 AA; 68851 MW; C48750B9F9E4EBDA CRC64;

Query Match 25.6%; Score 299; DB 1; Length 611;
Best Local Similarity 34.4%; Pred. No. 2.3e-20;
Matches 72; Conservative 28; Mismatches 89; Indels 20; Gaps 6;

Qy 13 LLLFLNTCLNGQLPPCK-----PEIFKCSPNKEHTCWRTGGLT-----PTNYSL 62
Db 6 LLLTLVLVCAVNDLSASDDVLRLPQISKCSPELETFCYW---TDGNFYNLSAPGTIQL 62
Qy 63 TYHREGETLMEHCDDYITGGNSCHFGQYTSWRTY-IMVNNATQMGSSPSDELYVDVT 121
Db 63 LYMKRDNEDWKECPDYITAGENSICYFNSTYSIWIPIYCVKLVNKDEV---PDEKCFSDV 118
Qy 122 YIVOPDPLELAVEKQPEDRKPY--LWIKWSPTLIDLTGWTLLYELRLKEPKAAEW 179
Db 119 EIVLPDPPVHLNWTLLNTSQTGHGDIQVRWDPPPTADVQKGWITLEYELQYKEVNETKW 178
Qy 180 EIHFAQQQTEFKILSLHPGQKYLVOVRECK 208
Db 179 KELEPRLSTWVPLVSLKIGRDYEVRSR 207

RESULT 13
GHR CHICK STANDARD; PRT; 608 AA.
AC Q02092;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).
DE GHR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

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RC	TISSUE=Liver;
RX	MEDLINE=91243665; PubMed=2036984;
RA	Burnside J., Liu S.S., Cogburn L.A.;
RT	"Molecular cloning of the chicken growth hormone receptor
RT	complementary deoxyribonucleic acid: mutation of the gene in
RT	sex-linked dwarf chickens."
RL	Endocrinology 128:3183-3192(1991).
CC	-I- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC	-I- SUBUNIT: Homodimer.
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-I- TISSUE SPECIFICITY: Broad specificity.
CC	-I- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC	Subfamily 1.
CC	-I- SIMILARITY: Contains 1 fibronectin type III domain.
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CC	or send an email to license@isb-sib.ch).
CC	-----
CC	EMBL; M74057; AAA48781.1; --
DR	PfR; S32823; S32823.
DR	HSP; P10912; IAXI.
DR	InterPro; IPRO02996; CR1A.
DR	InterPro; IPRO08957; FN_III-like.
DR	InterPro; IPRO03961; FN_III.
DR	InterPro; IPRO03528; Hemtopopn_L_Fl.
DR	Pfam; PF00041; fn3; 1.
DR	SMART; SM00060; FN3; 1.
DR	PROSITE; PS01352; HEMATOPO REC L F1; 1.
KW	Receptor; Transmembrane; Glycoprotein; Signal.
FT	SIGNAL 1 16 POTENTIAL.
FT	CHAIN 17 608 GROWTH HORMONE RECEPTOR.
FT	DOMAIN 17 237 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 238 261 POTENTIAL.
FT	DOMAIN 262 608 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 117 223 FIBRONECTIN TYPE-III.
FT	BY SIMILARITY.
FT	DISULFID 34 44 BY SIMILARITY.
FT	DISULFID 72 83 BY SIMILARITY.
FT	DISULFID 97 111 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE 608 AA; 68572 MW; D71AD7B6C62528DC CRC64;
Query Match	25.4%; Score 296; DB 1; Length 608;
Best Local Similarity	35.5%; Pred. No. 4.4e-20;
Matches	65; Conservative 30; Mismatches 76; Indels 12; Gaps 5;
QY	31 PEIFKCRSPNKETFTCWRRPGTDGGLPTN--YSLTYHREGETLMHECPDYITGGPNSCHF 88
Dd	29 PQISKCRSPELETSCYW--TDGKVITSGTIQLLYMKRSDEDKNKECFDYITAGENSICYF 85
QY	89 GKQYTSMMRTY-IMVYNATQMGSSFDELYVDVTYIVQDPDPLELAIVEVKQPERKY-- 145
Dd	86 NTSYTSIMIPYCVKLANDEV----FDEKCFSPVEIPLVPDPVHLNMTLNTSGIHGD 141
QY	146 LWIKWSPTLLDLKTGWFTFLAYELRKPEAAAEIHFAGQOTEFKILSLHPGOKYLQV 205
Dd	142 IQVRDDPPPTADVQKGWITILEYQYKVNENKWELEPRLSSTVVPLYSLNGRDYEIRV 201
QY	206 RCK 208
Dd	202 RSR 204
RESULT 14	
GHR RAT	STANDARD; PRT; 638 AA.
ID - GHR RAT	

```

Db 109 ANSCFFNSYSIWIPYCIKUTT---NGDLDEXFTVDEIVQDPPIGLNWTILNISLP 165
QY 140 EDRFYLWIKSPPTLIDKGTGFTLLYIEIRLKEPEKAAEWEIHPAGQOTEFKILSLHPGQ 199
Db 166 GIRGD-IQVSNQPPSADVLKGMWILEIYEQKEVETKWTMTSPITVSTVPLYSRLDK 224
QY 200 KYLVQVRCK 208
Db 225 EHEVRVRSR 233

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RESULT 15

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GHR_BOVIN
ID_GHR_BOVIN STANDARD; PRT; 634 AA.
AC P75I08;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
GN GHR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GR; TISSUE=Liver;
RA Souza S.C., Wang X., Lobo R.B., Knoch J.J.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

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EMBL: X70041; CAA49635.1; -.
DR HSSP; P10912; 1A22.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 19 634
FT DOMAIN 19 260
FT TRANSMEM 261 284
FT DOMAIN 285 634
FT DOMAIN 141 248
FT DISULFID 56 66
FT DISULFID 97 108
FT DISULFID 122 136
FT CARBOHYD 46 46
FT CARBOHYD 73 73
FT CARBOHYD 111 111
FT CARBOHYD 152 152
FT CARBOHYD 157 157
FT CARBOHYD 196 196
FT CARBOHYD 634 AA; 70979 MW; 91955A28296CBD2E CRC64;
SEQUENCE

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Query Match 24.9%; Score 290.5; DB 1; Length 634;
Best Local Similarity 34.6%; Pred. No. 1.5e-19;
Matches 64; Conservative 26; Mismatches 86; Indels 9; Gaps 4;
QY 29 GKPEIFKCRSPNKETFTCWWRPGTDGGL--PTNYSLTYYHREGETLMHCEPDYITGGPNSC 86
Db 49 GNPFTKCRSPELETFSCWTDGANHSLSQSPGVQMFYIRDDIQEWKECPDYVSAAGNSC 108
QY 87 HFGKQYTSNWRITYIMVNAVATQWGSFSDLYVDVTYIVQDPDPLEL---AVEVKQPDCK 143
Db 109 YFNSSYTSVWTPYCIKITS---NGIVDHKCFSEVDIVQDPDPPVGLNWTILNISLTHA 165
QY 144 PYLWIKSPPTLIDKGTGFTLLYIEIRLKEPEKAAEWEIHPAGQOTEFKILSLHPGQYLV 203
Db 166 DIL-VKWEPPPTNDVEMGMWILEYELHYKELNETQWQMDPLMVTSPMYSRLDKKEVEV 224
QY 204 QVRCK 208
Db 225 RVRTR 229

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Search completed: May 12, 2004, 16:17:57  
Job time : 18 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2004, 16:14:46 ; Search time 45 Seconds  
(without alignments)  
1472.418 Million cell updates/sec

Title: US-10-029-079-3  
Perfect score: 1166  
Sequence: 1 MKNVASATVFTLLFLNTC.....KILSLHPGQXLYVQRCKPD 210

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 135518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1155.5	99.1	268	4 Q8TD78	Q8td78 homo sapien
2	1155.5	99.1	288	4 Q96P36	Q96p36 homo sapien
3	1155.5	99.1	349	4 Q9UHJ5	Q9uhj5 homo sapien
4	1155.5	99.1	376	4 Q96P35	Q96p35 homo sapien
5	1088.5	93.4	622	6 Q85V4	Q85v4 cebus apell
6	1052.5	90.3	622	6 Q9N0J7	Q9n0j7 callithrix
7	1036.5	88.9	206	4 Q16354	Q16354 homo sapien
8	888.5	76.2	625	6 Q9XS92	Q9xs92 trichosurus
9	814.5	69.9	292	11 Q8C7G1	Q8c7g1 mus musculus
10	811.5	69.6	608	11 Q99J21	Q99j21 mus musculus
11	764.5	65.6	198	6 Q18985	Q18985 cervus elap
12	759.5	65.1	197	4 Q8TD76	Q8td76 homo sapien
13	759.5	65.1	217	4 Q8TD75	Q8td75 homo sapien
14	758.5	65.1	227	6 Q9GLW3	Q9glw3 ursus marit
15	691.5	59.3	460	13 Q7T220	Q7t220 gallus gall
16	683.5	58.6	217	6 Q46386	Q46386 mustela vis

#### ALIGNMENTS

RESULT 1

Q8TD78

ID Q8TD78 PRELIMINARY; PRT; 268 AA.

AC Q8TD78; 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Prolactin receptor delta 7/11.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Breast tumor;

RA Trott J.F., Hovey R.C., Koduri S., Vanderhaar B.K.;

RT "Expression of multiple human prolactin receptor variants in breast and colon cancer derived by splicing to exon 11.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF492470; AAM18048.1; -

DR GO; GO:0016020; C.membrane; IEA

DR GO; GO:0004896; F.hematopoietin/interferon-class (D200-domain. . . ; IEA.

DR GO; GO:0004872; F.receptor activity; IEA.

DR InterPro; IPR002996; CRA.

DR InterPro; IPR003961; FN.III.

DR InterPro; IPR008957; FN.III-like.

DR InterPro; IPR003528; Hemtopoptn\_L\_F1.

DR Pfam; PF00041; fn3; 2

DR SMART; SM00600; FN3; 2

DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.

SW SEQUENCE 268 AA; 30705 MW; FBB498AB649A078C CRC64;

Query Match 99.1%; Score 1155.5; DB 4; Length 268;

Best Local Similarity 99.5%; Pred. No. 6.6e-109;

Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MKNVASATVFTLLFLNTCLANGQIPPKRPEIFKCRSNKKTFTCWWRPGTDGGLPTNY 60

|||||

Q90WG7 cynops pyrr  
Q9ptn9 xenopus lae  
Q9ibf6 xenopus lae  
Q9pt10 xenopus lae  
Q9de08 oncorhynchu  
Q90zi6 paralichthy  
Q91404 oreochromis  
Q8G54 cyprinus ca  
Q9tp0 carassius a  
Q9dfu0 sparus aua  
O18853 mustela put  
Q9pt11 xenopus lae  
Q86xs2 homo sapien  
Q9ge35 pelodiscus  
Q9av08 columba liv  
Q95jf2 ailuropoda  
Q9uhf5 homo sapien  
Q9nu07 monodelphis  
Q75462 homo sapien  
Q9jkt1 cavia porce  
Q9jms8 mus musculu  
Q80xw9 rattus sp.  
Q9ji97 cavia porce  
O46600 bos taurus  
Q90z55 scophthalmu  
Q90z56 scophthalmu  
Q9jkg1 cavia porce  
Q90z50 carassius a  
Q7t3u1 ctenopharyn

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Db 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAVAT-QMGSSFSDELYVD 119
Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAVATQMGSSFSDELYVD 120
QY 120 VTYIVQDPDPPELEAVEVQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 179
Db 121 VTYIVQDPDPPELEAVEVQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 180
QY 180 EIHFAQQOTEFKILSLHFGQKYLQVVRCKPD 210
Db 181 EIHFAQQOTEFKILSLHFGQKYLQVVRCKPD 211

RESULT 2
Q96P36
ID Q96P36 PRELIMINARY; PRT; 288 AA.
AC Q96P36
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Prolactin receptor short isoform A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20054419; PubMed=10585417;
RA Kline J.B., Roehrs H., Clevenger C.V.;
RT "Functional characterization of the intermediate isoform of the human
RT prolactin receptor."
RL J. Biol. Chem. 274:35461-35468 (1999).
DR HSSP; P16471; 1BP3.
DR EMBL; AF166329; RAD49855.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR RECEPTOR.
KW Receptor.
SQ SEQUENCE 288 AA; 32760 MW; B45203EC045EB417 CRC64;

Query Match 99.1%; Score 1155.5; DB 4; Length 288;
Best Local Similarity 99.5%; Pred. No. 7.2e-109;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNY 60
Db 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAVAT-QMGSSFSDELYVD 119
Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAVATQMGSSFSDELYVD 120
QY 120 VTYIVQDPDPPELEAVEVQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 179
Db 121 VTYIVQDPDPPELEAVEVQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 180
QY 180 EIHFAQQOTEFKILSLHFGQKYLQVVRCKPD 210
Db 181 EIHFAQQOTEFKILSLHFGQKYLQVVRCKPD 211

RESULT 3
Q9UHJ5
ID Q9UHJ5 PRELIMINARY; PRT; 349 AA.

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AC Q9UHJ5;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Intermediate prolactin receptor isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20054419; PubMed=10585417;
RA Kline J.B., Roehrs H., Clevenger C.V.;
RT "Functional characterization of the intermediate isoform of the human
RT prolactin receptor."
RL J. Biol. Chem. 274:35461-35468 (1999).
DR HSSP; P16471; 1BP3.
DR EMBL; AF166329; RAD49855.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR RECEPTOR.
KW Receptor.
SQ SEQUENCE 349 AA; 39806 MW; 932F200E850CDD27 CRC64;

Query Match 99.1%; Score 1155.5; DB 4; Length 349;
Best Local Similarity 99.5%; Pred. No. 9.1e-109;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNY 60
Db 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAVAT-QMGSSFSDELYVD 119
Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAVATQMGSSFSDELYVD 120
QY 120 VTYIVQDPDPPELEAVEVQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 179
Db 121 VTYIVQDPDPPELEAVEVQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 180
QY 180 EIHFAQQOTEFKILSLHFGQKYLQVVRCKPD 210
Db 181 EIHFAQQOTEFKILSLHFGQKYLQVVRCKPD 211

RESULT 4
Q96P35
ID Q96P35 PRELIMINARY; PRT; 376 AA.
AC Q96P35;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Prolactin receptor short isoform B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA Trott J.F., Hovey R.C., Vonderhaar B.K.;
RT "Expression of two novel hPRLR isoforms in breast tumors."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416619; AAL23915.1; -.
DR PIR; A59405; A59405.

```

DR GO; GO:0016020; C-membrane; IEA.  
DR GO; GO:0004896; F.hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F.receptor activity; IEA.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 2.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor.  
SQ SEQUENCE 376 AA; 42639 MW; 112DC2555FBC4601 CRC64;  
  
Query Match 99.1%; Score 1155.5; DB 4; Length 376;  
Best Local Similarity 99.5%; Pred. No. 9.9e-109;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 MKENVASATVFTLLFLNTCLLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
Db 1 MKENVASATVFTLLFLNTCLLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
  
QY 61 SLTYHREGETLMHECPDYITGPNCHFGKQYTSMWRTYIMVNAT-QMGSSFSDELYVD 119  
Db 61 SLTYHREGETLMHECPDYITGPNCHFGKQYTSMWRTYIMVNAT-QMGSSFSDELYVD 120  
  
QY 120 VTYIVQPPPLELAVKQPEDKPYLWKSPPTLIDLTGWTLLYEIRLKPKEAAEW 179  
Db 121 VTYIVQPPPLELAVKQPEDKPYLWKSPPTLIDLTGWTLLYEIRLKPKEAAEW 180  
  
QY 180 EIHFAQQOTEFKILSLHPGQKYLQVVRCKPD 210  
Db 181 EIHFAQQOTEFKILSLHPGQKYLQVVRCKPD 211  
  
RESULT 5  
Q865V4 PRELIMINARY; PRT; 622 AA.  
ID Q865V4  
AC Q865V4;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Prolactin receptor long form.  
GN PRLR.  
OS Cebus apella (Brown-capped capuchin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.  
OX NCBI\_TaxID=9515;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rojas-Garcia P.P., Germain A., Torres-Parfan C.L., Richter H.G.,  
RA Campino C., Seron-Ferre M.J.;  
RT "Expression of prolactin (PRL) receptor in ovary of capuchin monkey.  
RT Initial studies."  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY227708; AAO73437.1; -.  
DR GO; GO:0016020; C-membrane; IEA.  
DR GO; GO:0004896; F.hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F.receptor activity; IEA.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 2.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor.  
SQ SEQUENCE 622 AA; 69597 MW; BF794773C1FCADB3 CRC64;  
  
Query Match 93.4%; Score 1088.5; DB 6; Length 622;  
Best Local Similarity 91.9%; Pred. No. 1.1e-101;  
Matches 194; Conservative 8; Mismatches 8; Indels 1; Gaps 1;  
  
QY 1 MKENVASATVFTLLFLNTCLLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60

Db 1 MKENVASATVFTLLFLNTCLLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
  
QY 61 SLTYHREGETLMHECPDYITGPNCHFGKQYTSMWRTYIMVNAT-QMGSSFSDELYVD 119  
Db 61 SLTYHREGETLMHECPDYITGPNCHFGKQYTSMWRTYIMVNAT-QMGSSFSDELYVD 120  
  
QY 120 VTYIVQPPPLELAVKQPEDKPYLWKSPPTLIDLTGWTLLYEIRLKPKEAAEW 179  
Db 121 VTYIVQPPPLELAVKQPEDKPYLWKSPPTLIDLTGWTLLYEIRLKPKEAAEW 180  
  
QY 180 EIHFAQQOTEFKILSLHPGQKYLQVVRCKPD 210  
Db 181 EIHFAQQOTEFKILSLHPGQKYLQVVRCKPD 211  
  
RESULT 6  
Q9NOJ7 PRELIMINARY; PRT; 622 AA.  
ID Q9NOJ7  
AC Q9NOJ7;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Prolactin receptor precursor.  
OS Callithrix jacchus (Common marmoset).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.  
OX NCBI\_TaxID=9483;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20457117; PubMed=11000523;  
RA Daltymple A., Edery M., Jabbour H.;  
RT "Sequence and functional characterization of the marmoset monkey  
RT (Callithrix jacchus) prolactin receptor: comparative homology with the  
RT human long-form prolactin receptor.;"  
RL Mol. Cell. Endocrinol. 167:89-97(2000).  
DR EMBL; AJ272217; CAB75847.1; -.  
DR HSSP; P16471; 1BP3.  
DR GO; GO:0016020; C-membrane; IEA.  
DR GO; GO:0004896; F.hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F.receptor activity; IEA.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 2.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor; Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 622 PROLACTIN RECEPTOR.  
SQ SEQUENCE 622 AA; 69425 MW; 65F99522C6CD6DB6 CRC64;  
  
Query Match 90.3%; Score 1052.5; DB 6; Length 622;  
Best Local Similarity 87.2%; Pred. No. 5.1e-98;  
Matches 184; Conservative 13; Mismatches 13; Indels 1; Gaps 1;  
  
QY 1 MKENVASATVFTLLFLNTCLLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
Db 1 MKENVASATVFTLLFLNTCLLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
  
QY 61 SLTYHREGETLMHECPDYITGPNCHFGKQYTSMWRTYIMVNAT-QMGSSFSDELYVD 119  
Db 61 SLTYHREGETLMHECPDYITGPNCHFGKQYTSMWRTYIMVNAT-QMGSSFSDELYVD 120  
  
QY 120 VTYIVQPPPLELAVKQPEDKPYLWKSPPTLIDLTGWTLLYEIRLKPKEAAEW 179  
Db 121 VTYIVQPPPLELAVKQPEDKPYLWKSPPTLIDLTGWTLLYEIRLKPKEAAEW 180  
  
QY 180 EIHFAQQOTEFKILSLHPGQKYLQVVRCKPD 210  
Db 181 EIHFAQQOTEFKILSLHPGQKYLQVVRCKPD 211

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RESULT 7
ID Q16354 PRELIMINARY; PRT; 206 AA.
AC Q16354;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Prolactin receptor (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95286597; PubMed=7768908;
RA Fuh G., Wells J.A.;
RT "Prolactin receptor antagonists that inhibit the growth of breast
RT cancer cell lines.";
RL J. Biol. Chem. 270:13133-13137(1995).
DR EMBL; S78505; AAB34470.1; -.
DR HSP; P16471; IBP3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR Receptor.
KW NON-TER.
FT CHAIN 1 24
FT SIGNAL 25 625
FT POTENTIAL
FT PROLACTIN RECEPTOR.
SQ SEQUENCE 206 AA; 23950 MW; CED939781B3C804E CRC64;

Query Match 88.9%; Score 1036.5; DB 4; Length 206;
Best Local Similarity 99.5%; Pred. No. 5.6e-97;
Matches 186; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 25 QLPKPKETFKCRSPKSTFTCWRRPGTGGLPNYSITVHREGTLMHCEPDYITGGPN 84.
DB 1 QLPKPKETFKCRSPKSTFTCWRRPGTGGLPNYSITVHREGTLMHCEPDYITGGPN 60

QY 85 SCHFGKQYTMWRTYIMVNAT-QMGSSFSDELIVDTYIVQDPDPLEAVEVKQPEDRK 143
DB 61 SCHFGKQYTMWRTYIMVNATQMGSSFSDELIVDTYIVQDPDPLEAVEVKQPEDRK 120

QY 144 PYLWIKWSPPTLIDLTGWFLLYEIRLKPKEAAEWIHFAGQOTEFKILSLHPGOKYLV 203
DB 121 PYLWIKWSPPTLIDLTGWFLLYEIRLKPKEAAEWIHFAGQOTEFKILSLHPGOKYLV 180

QY 204 QVRCKPD 210
DB 181 QVRCKPD 187

RESULT 8
Q9XS92 PRELIMINARY; PRT; 625 AA.
ID Q9XS92;
AC Q9XS92;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Prolactin receptor precursor.
OS PRL-8.
OC Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
[1]
RP SEQUENCE FROM N.A.
RX TISSUE=Testis;
RA MEDLINE=99236966; PubMed=10221777;

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RA Demmer J.;
RT "The prolactin receptor from the brushtail possum (Trichosurus
RT vulpecula): cDNA cloning, expression and functional analysis.";
RL Mol. Cell. Endocrinol. 148:119-127(1999).
DR EMBL; AF098296; AAD27039.1; -.
DR HSP; P16471; IBP3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR008957; FN.III-like.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR Receptor; Signal.
KW SIGNAL 1 24
KW POTENTIAL
FT CHAIN 25 625
FT PROLACTIN RECEPTOR.
SQ SEQUENCE 625 AA; 70539 MW; 2097D72827C9DB6 CRC64;

Query Match 76.2%; Score 888.5; DB 6; Length 625;
Best Local Similarity 73.9%; Pred. No. 2.2e-81;
Matches 156; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLANGQLPPGKPEIFKCRSPKSTFTCWRRPGTGGLPNTY 60
DB 1 MKNVTSATAPLFLHLLHLLHLLHLLHLLHLLHLLHLLHLLHLLHLLHLLHLLHLLH 60

QY 61 SLTYHREGTLMHCEPDYITGGPNSCHFGKQYTMWRTYIMVNAT-QMGSSFSDELIVDT 119
DB 61 TLFYRKEGESLTHCEPDYITGGPNSCHFGKQYTMWRTYIMVNATQMGSSFSDELIVDT 120

QY 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWIKWSPPTLIDLTGWFLLYEIRLKPKEAAEW 179
DB 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWIKWSPPTLIDLTGWFLLYEIRLKPKEAAEW 180

QY 180 EHFAGQOTEFKILSLHPGOKYLVQVRCKPD 210
DB 181 EHFAGQOTEFKILSLHPGOKYLVQVRCKPD 211

RESULT 9
Q8C7G1 PRELIMINARY; PRT; 292 AA.
ID Q8C7G1;
AC Q8C7G1;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Prolactin receptor related sequence 1.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK050317; BAC34185.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR008957; FN.III-like.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.

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SQ SEQUENCE 292 AA; 33618 MW; 9D60422B59E88A19 CRC64;
Query Match 69.9%; Score 814.5; DB 11; Length 292;
Best Local Similarity 69.8%; Pred. No. 2.8e-74;
Matches 143; Conservative 25; Mismatches 36; Indels 1; Gaps 1;

QY 7 SATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTTHR 66
DB 2 SSALAYNLLVLSISLLNGQSPGKPEIHKCRSPDKETFTCWWRPGSDGGLPTNYSLSYK 61
QY 67 EGTLMHECDPYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTVIVQ 125
DB 62 EGEKNTYECDPYKTSFGNSCFKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTVIVVE 121
QY 126 PDPELEAVEVKQPEDEKPKYLMWKSPPTLIDLTGFTLLYIRLKPAAAEWEIHFAG 185
DB 122 PEPRNLTLVQKVKQKXTLWKLWLPPTITDVKTGFTMEYERLKSSEADEWEIHFAG 181
QY 186 QOTEFKLSLHPGQKYLQVRCRKP 210
DB 182 HQTQKVFVLYPGQKYLQVTRCKPD 206

RESULT 10
Q99JZ1 PRELIMINARY; PRT; 608 AA.
AC Q99JZ1;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Prolactin receptor.
GN PRLR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005555; AA05555.1; -.
DR EMBL; BC006652; AA06652.1; -.
DR HSSP; P16471; 1BP3.
DR MGB; MGI:97763; Prlr.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III-like.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor.
SQ SEQUENCE 608 AA; 68223 MW; 2710DAEC2B1A8F63 CRC64;

Query Match 69.6%; Score 811.5; DB 11; Length 608;
Best Local Similarity 71.4%; Pred. No. 1.4e-73;
Matches 142; Conservative 23; Mismatches 33; Indels 1; Gaps 1;

QY 13 LLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTTHREGFTLM 72
DB 8 MLLVLSISLLNGQSPGKPEIHKCRSPDKETFTCWWRPGSDGGLPTNYSLSYKEGKNT 67
QY 73 HECDPYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTVIVQDPDPLE 131
DB 68 YECDPYKTSFGNSCFKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTVIVVEPEPPRN 127
QY 132 LAVEVKQPEDEKPKYLMWKSPPTLIDLTGFTLLYIRLKPAAAEWEIHFAGQOTEFK 191
DB 128 LLELVQLKDKXTYLWKLWLPPTITDVKTGFTMEYERLKSSEADEWEIHFAGTQTFK 187
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QY 192 ILSLHPGQKYLQVRCRKP 210
DB 188 VFDLYPGQKYLQVTRCKPD 206

RESULT 11
Q18985 PRELIMINARY; PRT; 198 AA.
AC Q18985;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Soluble prolactin receptor.
GN PROLACTIN RECEPTOR.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98389256; PubMed=9723863;
RA Jabbour H.N.; Clarke L.A.; Bramley T.; Postal-Vinay M.C.; Kelly P.A.;
RA Edery M.;
RT "Alternative splicing of the prolactin receptor gene generates a 1.7
RT kb RNA transcript that is linked to prolactin function in the red deer
RT testis."
RL J. Mol. Endocrinol. 21:51-59(1998).
DR EMBL; Y14753; CAA75048.1; -.
DR HSSP; P16471; 1BP3.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III-like.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 198 AA; 22652 MW; C020E070D970AC40 CRC64;

Query Match 65.6%; Score 764.5; DB 6; Length 198;
Best Local Similarity 72.9%; Pred. No. 2.1e-69;
Matches 132; Conservative 21; Mismatches 27; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
DB 1 MKENVASRAVFTLLFLNASLLNGQSPGKPKIICRSPGKETFTCWWRPGSDGGLPTNY 60
QY 61 SLTYHREGTLMHECDPYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVD 119
DB 61 TLTYHKEGETLHIECDPYITGGPNTCYFSKHTSIWKIIVITVAINQMGVSSDPLYVD 120
QY 120 VTIVQDPDPELEAVEVKQPEDEKPKYLMWKSPPTLIDLTGFTLLYIRLKPAAAEW 179
DB 121 VTIVVEPEPPANTLELKHEDKPKYLMWKSPPTLIDLVKSGWFMFIQYERLKPETATOW 180
QY 180 E 180
DB 181 E 181

RESULT 12
Q8TD76 PRELIMINARY; PRT; 197 AA.
ID Q8TD76
AC Q8TD76;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Delta 4-delta 7/11 truncated prolactin receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.  
RC TISSUE=Breast tumor;  
RA Trotter J.F., Hovey R.C., Koduri S., Vonderhaar B.K.;  
RT "Expression of multiple human prolactin receptor variants in breast  
and colon cancer derived by splicing to exon 11."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF493068; AAM11660.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003961; FN.III.  
DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
DR KW Receptor.  
SQ SEQUENCE 197 AA; 22718 MW; D916BC915621EEEF CRC64;  
Query Match 65.1%; Score 759.5; DB 4; Length 197;  
Best Local Similarity 99.3%; Pred. No. 6.6e-69;  
Matches 139; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 72 MHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTVYIVQDPPL 130  
DB 1 MHECPDYITGGPNSCHFGKQYTSWRTYIMVNATQMGSSFSDELYVDVTVYIVQDPPL 60  
QY 131 ELAVEVKQPEDRKPYLWIKWSPPTLIDLTGFTLLYEIRLKPKEAAEWEIHFAQQOTEF 190  
DB 61 ELAVEVKQPEDRKPYLWIKWSPPTLIDLTGFTLLYEIRLKPKEAAEWEIHFAQQOTEF 120  
QY 191 KILSLHPGQKYLQVRCRCPD 210  
DB 121 KILSLHPGQKYLQVRCRCPD 140  
RESULT 13  
Q8TD75 ID Q8TD75 PRELIMINARY; PRT; 217 AA.  
AC Q8TD75  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Delta 4-Sf1b truncated prolactin receptor.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Breast tumor;  
RA Trotter J.F., Hovey R.C., Koduri S., Vonderhaar B.K.;  
RT "Expression of multiple human prolactin receptor variants in breast  
and colon cancer derived by splicing to exon 11."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF493068; AAM11660.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003961; FN.III.  
DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
DR KW Receptor.  
SQ SEQUENCE 217 AA; 24773 MW; E59A9BB9016C3397 CRC64;  
Query Match 65.1%; Score 759.5; DB 4; Length 217;  
Best Local Similarity 99.3%; Pred. No. 7.4e-69;  
Matches 139; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 72 MHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDVTVYIVQDPPL 130  
DB 1 MHECPDYITGGPNSCHFGKQYTSWRTYIMVNATQMGSSFSDELYVDVTVYIVQDPPL 60  
RESULT 14  
Q9GLW3 ID Q9GLW3 PRELIMINARY; PRT; 227 AA.  
AC Q9GLW3  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Prolactin receptor (Fragment).  
OS Ursus maritimus (Polar bear) (Thalactos maritimus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.  
CX NCBI\_TaxID=29073;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=20086658; PubMed=10618652;  
RA Howell-Skalla L.A., Bunick D., Bleck G.T., Nelson R.A., Bahr J.M.;  
RT "Cloning and sequence analysis of the extracellular region of the  
polar bear (Ursus maritimus) luteinizing hormone receptor (LHR),  
RT follicle stimulating hormone receptor (FSHR), and prolactin receptor  
RT (Prlr) genes and their expression in the testis of the black bear  
RT (Ursus americanus).";  
RL Mol. Reprod. Dev. 55:136-145 (2000).  
DR EMBL; AF189792; AAG10648.1; -  
DR HSPF; PF6471; IIP3.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR002996; CRI1.  
DR InterPro; IPR003961; FN.III.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
DR Receptor.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 227 227  
SQ SEQUENCE 227 AA; 26114 MW; F5E6C5F33B5D5B49 CRC64;  
Query Match 65.1%; Score 758.5; DB 6; Length 227;  
Best Local Similarity 75.4%; Pred. No. 9.8e-69;  
Matches 129; Conservative 22; Mismatches 19; Indels 1; Gaps 1;  
QY 41 KETFTCWRRPGTGGTGYNTYSLYTHREGETLMECPDYITGGPNSCHFGKQYTSWRTYI 100  
DB 1 KETFTCWRRPGTGGTGYNTYSLYTHREGETLMECPDYITGGPNSCHFGKQYTSWRTYI 60  
QY 101 MYVNAT-QMGSSFSDELYVDVTVYIVQDPPL-ELAVEVKQPEDRKPYLWIKWSPPTLIDLK 159  
DB 61 ITNATQMGSSFSDELYVDVTVYIVQDPPL-ELAVEVKQPEDRKPYLWIKWSPPTLIDLK 120  
QY 160 TGMFTLLYEIRLKPKEAAEWEIHFAQQOTEFKILSLHPGQKYLQVRCRCPD 210  
DB 121 SGWLTLLQEIRLKPKEATETWETHFAQQOTQFKILSLHPGQKYLQVRCRCPD 171  
RESULT 15  
Q7T2Z0 ID Q7T2Z0 PRELIMINARY; PRT; 460 AA.  
AC Q7T2Z0  
DT 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Prolactin receptor (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

QY 131 ELAVEVKQPEDRKPYLWIKWSPPTLIDLTGFTLLYEIRLKPKEAAEWEIHFAQQOTEF 190  
DB 61 ELAVEVKQPEDRKPYLWIKWSPPTLIDLTGFTLLYEIRLKPKEAAEWEIHFAQQOTEF 120  
QY 191 KILSLHPGQKYLQVRCRCPD 210  
DB 121 KILSLHPGQKYLQVRCRCPD 140  
RESULT 14  
Q9GLW3 ID Q9GLW3 PRELIMINARY; PRT; 227 AA.  
AC Q9GLW3  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Prolactin receptor (Fragment).  
OS Ursus maritimus (Polar bear) (Thalactos maritimus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.  
CX NCBI\_TaxID=29073;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=20086658; PubMed=10618652;  
RA Howell-Skalla L.A., Bunick D., Bleck G.T., Nelson R.A., Bahr J.M.;  
RT "Cloning and sequence analysis of the extracellular region of the  
polar bear (Ursus maritimus) luteinizing hormone receptor (LHR),  
RT follicle stimulating hormone receptor (FSHR), and prolactin receptor  
RT (Prlr) genes and their expression in the testis of the black bear  
RT (Ursus americanus).";  
RL Mol. Reprod. Dev. 55:136-145 (2000).  
DR EMBL; AF189792; AAG10648.1; -  
DR HSPF; PF6471; IIP3.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR002996; CRI1.  
DR InterPro; IPR003961; FN.III.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SM00060; FN3; 1.  
DR Receptor.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 227 227  
SQ SEQUENCE 227 AA; 26114 MW; F5E6C5F33B5D5B49 CRC64;

QY 41 KETFTCWRRPGTGGTGYNTYSLYTHREGETLMECPDYITGGPNSCHFGKQYTSWRTYI 100  
DB 1 KETFTCWRRPGTGGTGYNTYSLYTHREGETLMECPDYITGGPNSCHFGKQYTSWRTYI 60  
QY 101 MYVNAT-QMGSSFSDELYVDVTVYIVQDPPL-ELAVEVKQPEDRKPYLWIKWSPPTLIDLK 159  
DB 61 ITNATQMGSSFSDELYVDVTVYIVQDPPL-ELAVEVKQPEDRKPYLWIKWSPPTLIDLK 120  
QY 160 TGMFTLLYEIRLKPKEAAEWEIHFAQQOTEFKILSLHPGQKYLQVRCRCPD 210  
DB 121 SGWLTLLQEIRLKPKEATETWETHFAQQOTQFKILSLHPGQKYLQVRCRCPD 171  
RESULT 15  
Q7T2Z0 ID Q7T2Z0 PRELIMINARY; PRT; 460 AA.  
AC Q7T2Z0  
DT 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Prolactin receptor (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

Thu May 13 08:55:53 2004

```
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Hui A.M.Y., Leung F.C.;
RT "Genomic characterization of chicken prolactin receptor gene.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AV237376; AAP49452.1; -.
KW Receptor.
FT NON_TER 460 460
SQ SEQUENCE 460 AA; 52901 MW; 947DA92892A19361 CRC64;

Query Match 59.3%; Score 691.5; DB 13; Length 460;
Best Local Similarity 62.4%; Pred. No. 1.4e-61;
Matches 118; Conservative 31; Mismatches 39; Indels 1; Gaps 1;

QY 23 NGQLPRGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSILYHREGETLMHECPDYITGG 82
Db 226 SGQSPPEKPTIIKCRSPEKETFTCWWRPGLDGGHPNYILLYSREGEEQVYECPDYRTAG 285

QY 83 PNSCHFGKQVTSMMRTYIMVNAT-QWGSSFSDXLVDVTYIVQDPPLLEAVEVKQPED 141
Db 286 PNSCYFDKHTSFWTIYNITVRATNENGSSDPHYVDVTYIVQDPVPVNVITLKKPIN 345

QY 142 RKPVLWKWSPPTLIDLKTGNFTLLYHRLKPKAAWEIHFAGQOTEPKILSLHFGQKY 201
Db 346 RKPVLVLTWSPPLADVRSGLTLEYELRLKPEEGEWEETIFVGQOTQYKMFSLNPKKY 405

QY 202 LVQVRCKPD 210
Db 406 IIQHCKPD 414
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Search completed: May 12, 2004, 16:18:55  
Job time : 46 secs

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